

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:02:37 ; Search time 20 Seconds

(without alignments)

1885.354 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 2018

Sequence: 1 MDLFGDLPEPERSRPAAGK.....KAVQGSADNVTVMVVRIGH 392

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	481	23.8	341	2 G86315	hypothetical prote
2	474	23.5	242	2 T18588	probable protein p
3	401.5	19.9	300	2 A5804	phosphoprotein pho
4	370.5	18.4	414	2 S62462	protein phosphatas
5	368	18.2	389	2 T05095	hypothetical prote
6	368	18.2	975	2 T08606	protein phosphatas
7	365	18.1	359	2 T52337	phosphoprotein pho
8	364.5	18.1	348	2 T50783	protein phosphatas
9	362	17.9	464	2 H96700	protein F12A21.5 I
10	358.5	17.8	361	2 T45778	protein phosphatas
11	353.5	17.5	355	2 H84643	probable protein p
12	352.5	17.5	434	2 T04263	phosphoprotein pho
13	352	17.4	392	2 F84650	probable protein p
14	351	17.4	404	2 T00750	probable protein p
15	350	17.3	357	2 T06308	protein phosphatas
16	348	17.2	370	2 S54297	protein phosphatas
17	347	17.2	348	2 E89434	protein T23F11.1 I
18	347	17.2	356	2 T55181	hypothetical prote
19	340	16.8	382	2 S2422	phosphoprotein pho
20	340	16.8	382	2 A32399	phosphoprotein pho
21	338.5	16.8	383	2 T48018	hypothetical prote
22	338.5	16.8	390	2 C84826	protein phosphatas
23	338.5	16.8	405	2 F86206	hypothetical prote
24	338	16.7	382	2 I53823	magnesium dependen
25	337.5	16.7	380	2 E84748	probable protein p
26	336.5	16.7	381	2 T09640	protein phosphatas
27	336.5	16.7	396	2 T02483	probable protein p
28	336	16.7	382	2 S22423	phosphoprotein pho
29	336	16.2	390	2 S65672	phosphoprotein pho

30	326	16.2	393	2 I49016	phosphoprotein pho
31	321.5	15.9	442	2 B86209	protein F22G5.22 I
32	319	15.8	390	2 S20392	phosphoprotein pho
33	319	15.8	397	2 J25224	phosphoprotein pho
34	317.5	15.7	281	2 S41854	phosphoprotein pho
35	309	15.3	468	2 T21331	hypothetical prote
36	307	15.2	816	2 T48123	hypothetical prote
37	306	15.2	347	2 A56058	phosphoprotein pho
38	305.5	15.1	464	2 S50592	hypothetical prote
39	305	15.1	388	2 C85323	protein phosphatas
40	302	15.0	386	2 T09019	phosphoprotein pho
41	300	14.9	491	2 T16354	hypothetical prote
42	297	14.7	423	2 T48121	hypothetical prote
43	292.5	14.5	511	2 F96752	protein phosphatas
44	289	14.3	468	2 S39832	probable phosphopr
45	284	14.1	362	2 F84695	probable protein p

ALIGNMENTS

RESULT 1

G86315
hypothetical protein T10F20.4 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: G86315
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.X.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86315
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-341 <STO>
A;Cross-references: GB:AE005172; NID:g9719738; PIDN:AAF97840.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

Query Match 23.8%; Score 481; DB 2; Length 341;
Best Local Similarity 35.8%; Pred. No. 9.2e-28;
Matches 119; Conservative 66; Mismatches 107; Indels 40; Gaps 11;

QY 78 KRKTSEKNGSELY-----EKKVCKAGSVI-----FGLKGYVAERKGERBEMQDAHYI 127
DB 24 KAKKSEVSGGGEAVAAVGNREABEDKPSFVSEKKEFLVEADVAEDKGAHTMEDVWV 83
QY 128 LNDITBECRPPSSLIIRVSFVAVFDGHHGIRASKPAQNLHQNLRKPKGDVISYEKTV 187
DB 84 LPASLDF--PGTL--RCAHFAIYDGGGRLAAEFAKHLHLNLSAGLPRELLDV-KVA 138
QY 188 KRCLLTFKHTDEEFKQASSQKPAWKQSTATCVLAVNLIYIANLGSRAILCR---- 243
DB 139 KKAILEGFRKTDLLQLQKSVS--GGWQDGATAVCVWILDQKVFVANIGAKAVLAESST 196
QY 244 -----YNESQKHAALSLSKEHNPTQYERMRKQAGNV-RDGRVLGLVLSRSGIDGQ 297
DB 197 NELGNHTEAGNPLKATVLTREHKAITYPQBSRISQKSGGVSSNGRLQGRLVSRATGDRH 256
QY 298 YKCGVTSVPDIRRCOLLTNDREFILLACDGLFKVFTPEEAVNFIPLSCLEDEKIQTEGKS 357
DB 257 FKFGVGSATPDIIHAFELTRENFWLGGDLNEVFPSPDAVGFFVQKLL-----KEG-- 307
QY 358 AADARVEAACNRLANKAV-QRGSADNVTVMVV 388
DB 308 ---LHVSTVSVRLVKEAVKERRCKNCTAIVI 336

C;Keywords: phosphoric monoester hydrolase

Query Match 19.9%; Score 401.5; DB 2; Length 300;
Best Local Similarity 33.0%; Pred. No. 5.2e-22;
Matches 102; Conservative 53; Mismatches 105; Indels 49; Gaps 9;
QY 99 KASVIFGLKGYVAERKGEREEMODAHVILNDITECRPSSLLITRVSVFAVDPDGGGIR 158
D 18 QGKSVIFA-----ASEMCGWRNTMEDAHIRHDIQD-----VSVFGVDPDGGGIRE 63
QY 159 ASKFAAQNHLQNLII--RKPKGDVISVEKTVKRCCLDTFKHGTDEEFL-----KQASSQKP 211
D 64 VAQFVEKHFDVDELLKKNFK-----EKFEEALKETFLKMDLELLTPEGQKELAQYKA 116
QY 212 AWKD---GSTATCVLAVDNILYIANLGDSRAILCRYNESQKHAALSLSKENPTQYEE 267
D 117 TDTDESAGCTANVALLIYKNTLVANAGDSRSVLCRNNTNH-----DMSVDHKPDNPEE 170
QY 268 RMRQKAGNVRDGRVLGVLEVSRSIGDQYKRCG-----VTSVPDIRRCQLTPNDR 319
D 171 KSRIERAGGFSVSDGRVNGNLNLSRALGDLVEYKFDNKLRSNEQIIIALPDVKYKTELPQDK 230
QY 320 FILLACDGLFKVTPPEAVNFILSCLEDEKIQREKSAADARYEAACNRLANKAVQSGS 379
D 231 FILMGCDGVFETTLNHOELLKQVNSTIGQAOVTBELLKAAE-----DLDDQLLAPDTSQGTG 287
QY 380 ADNVTVMWV 388
D 288 CDNMTTILV 296
RESULT 4
S62462
Protein phosphatase 2c homolog 3 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 15-Jun-2001
C;Accession: T38573; S54298; S62462
R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z21745
A;Accession: T38573
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-414 <BA2>
A;Cross-references: EMBL:Z54354; NID:G1019398; PIDN:CAA91172.1; PID:G1019405; GSPDB:GNC
A;Experimental source: strain 972h-; cosmid C2G11
R;Shiozaki, K.; Russell, P.
EMBO J. 14, 492-502, 1995
A;Title: Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase kinase
A;Reference number: S54297; MUID:95163582; PMID:7859738
A;Accession: S54298
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-195, 'T', 197-414 <SHI>
A;Cross-references: EMBL:L34882; NID:G609657; PIDN:AAA67321.1; PID:G609658
C;Genetics:
A;Gene: SPAC2G11.07c
A;Map position: 1L
A;Introns: 110/1; 134/3
C;Superfamily: human phosphoprotein phosphatase 1A
Query Match 18.4%; Score 370.5; DB 2; Length 414;
Best Local Similarity 32.9%; Pred. No. 1.5e-19;
Matches 108; Conservative 53; Mismatches 100; Indels 67; Gaps 13;
QY 81 TSEEKNGSELVEKVKYKASSVIFGLKGYVAERKGEREEMODAHVILNDITECRPSS 140
D 10 TEKHSVNGSNEF-----VLYGL-----SSVQGWRIEMDAHSAL--LSMEC---SA 50
QY 141 LITRVSVFAVDPDGGGIRASKFAAQNHLQNLIRK--FPKGDVTSVEKTVKRCCLDT 194
D 51 VKDPVDVFAVYDGGGDKVAKWCGSNLPQILEKNPDKGDFVNAKSSFLNADKALID- 109
A;Genetic code: SGCS

C;Keywords: phosphoric monoester hydrolase
Query Match 19.9%; Score 401.5; DB 2; Length 300;
Best Local Similarity 33.0%; Pred. No. 5.2e-22;
Matches 102; Conservative 53; Mismatches 105; Indels 49; Gaps 9;
QY 99 KASVIFGLKGYVAERKGEREEMODAHVILNDITECRPSSLLITRVSVFAVDPDGGGIR 158
D 18 QGKSVIFA-----ASEMCGWRNTMEDAHIRHDIQD-----VSVFGVDPDGGGIRE 63
QY 159 ASKFAAQNHLQNLII--RKPKGDVISVEKTVKRCCLDTFKHGTDEEFL-----KQASSQKP 211
D 64 VAQFVEKHFDVDELLKKNFK-----EKFEEALKETFLKMDLELLTPEGQKELAQYKA 116
QY 212 AWKD---GSTATCVLAVDNILYIANLGDSRAILCRYNESQKHAALSLSKENPTQYEE 267
D 117 TDTDESAGCTANVALLIYKNTLVANAGDSRSVLCRNNTNH-----DMSVDHKPDNPEE 170
QY 268 RMRQKAGNVRDGRVLGVLEVSRSIGDQYKRCG-----VTSVPDIRRCQLTPNDR 319
D 171 KSRIERAGGFSVSDGRVNGNLNLSRALGDLVEYKFDNKLRSNEQIIIALPDVKYKTELPQDK 230
QY 320 FILLACDGLFKVTPPEAVNFILSCLEDEKIQREKSAADARYEAACNRLANKAVQSGS 379
D 231 FILMGCDGVFETTLNHOELLKQVNSTIGQAOVTBELLKAAE-----DLDDQLLAPDTSQGTG 287
QY 380 ADNVTVMWV 388
D 288 CDNMTTILV 296
RESULT 4
S62462
Protein phosphatase 2c homolog 3 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 15-Jun-2001
C;Accession: T38573; S54298; S62462
R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z21745
A;Accession: T38573
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-414 <BA2>
A;Cross-references: EMBL:Z54354; NID:G1019398; PIDN:CAA91172.1; PID:G1019405; GSPDB:GNC
A;Experimental source: strain 972h-; cosmid C2G11
R;Shiozaki, K.; Russell, P.
EMBO J. 14, 492-502, 1995
A;Title: Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase kinase
A;Reference number: S54297; MUID:95163582; PMID:7859738
A;Accession: S54298
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-195, 'T', 197-414 <SHI>
A;Cross-references: EMBL:L34882; NID:G609657; PIDN:AAA67321.1; PID:G609658
C;Genetics:
A;Gene: SPAC2G11.07c
A;Map position: 1L
A;Introns: 110/1; 134/3
C;Superfamily: human phosphoprotein phosphatase 1A
Query Match 18.4%; Score 370.5; DB 2; Length 414;
Best Local Similarity 32.9%; Pred. No. 1.5e-19;
Matches 108; Conservative 53; Mismatches 100; Indels 67; Gaps 13;
QY 81 TSEEKNGSELVEKVKYKASSVIFGLKGYVAERKGEREEMODAHVILNDITECRPSS 140
D 10 TEKHSVNGSNEF-----VLYGL-----SSVQGWRIEMDAHSAL--LSMEC---SA 50
QY 141 LITRVSVFAVDPDGGGIRASKFAAQNHLQNLIRK--FPKGDVTSVEKTVKRCCLDT 194
D 51 VKDPVDVFAVYDGGGDKVAKWCGSNLPQILEKNPDKGDFVNAKSSFLNADKALID- 109
A;Genetic code: SGCS

195 FKHTDEFLKQASSQKPAWKDGGTATCVLAVDNILYIANLGDRAILCRVNEESQKHAAL 254
110 ----DDQFHTDPS-----GCTATVLRVGNKLYCANAGDSRTVL-----GSKGIK 151
255 SLSEKHNPTQYERMRIOKAGNVDRGVLGVLEVSRSIGDGQYKRCG-----VTSVP 307
152 PLSADHKFESNAEKARICAGGVDGFRVGNLALSRAIGDFEFKSNLEPEKQIVTALP 211
308 DIRRCQTPNDRFTLLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAADARVEAA- 366
212 DVVVEITDDDEFVLVACDGIWCKTSQVIEFV-----RGI VAGTSLEKIAE 260
367 ---CNRLANKAVQRG-SADNVTVMVVRI 390
261 NLMNCIASDTETTLGLGCDNMTVCIVAL 288

RESULT 5
T05095
hypothetical protein F28M20.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C:Accession: T05095
R:Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes,
submitted to the Protein Sequence Database, November 1998
A:Reference number: 215398
A:Accession: T05095
A:Molecule type: DNA
A:Residues: 1-389 <BEV>
A:Cross-references: EMBL:AL031004
A:Experimental source: cultivar Columbia; BAC clone F28M20
C:Genetics:
A:Map position: 4
A:Introns: 95/1; 128/1; 181/1; 210/1; 274/3; 318/3
A:Note: F28M20.60
C:Superfamily: human phosphoprotein phosphatase 1A

Query Match 18.2%; Score 368; DB 2; Length 389;
Best Local Similarity 33.7%; Pred. No. 2.1e-19;
Matches 114; Conservative 40; Mismatches 86; Indels 98; Gaps 14;

109 GYVAERGEREMQDAHVILNDITEECRPPSSILTRVSYPAVFDGHHGIRASKFAAQNHL 168
60 GY-ASSPGKRSMEFVETRIDGVEG-----EIVGLFVGFDGHHGARAAYVRKNLF 110
169 QNLIRKFPKGDVISVETKVRCLDTFKHTDEFLKQASSQKPAWKD-GSTATCVLAVDN 227
111 SNLIR-HPK--FIS---DTTAAIADAVNQTDFELKSENQON---RDAGSTASTAILVGD 161
228 ILYIANLGDRAILCRVNEESQKHAALSLSKEHNPTQYERMRIOKAGNVDR---DGRVL 284
162 RLLVANVGDSSRAVICRGN-----ATAVSRDHKPDQSDERQRIEDAGGFVWAGTWVRG 215
285 GVLEVSRSIGDGQYKRCGTVSPDIR-----FILLACDGLFKVFTPEEAVNFILSCLEDEKIQ 351
216 GVLAVSRAFGDRLLKQY-VWADPETQVLTFCQNLVKNATLLTIEHNLHWISVSYL 274
311 -----RCQLTNDR-----FILLACDGLFKVFTPEEAVNFILSCLEDEKIQ 351
275 NGTLQNFLRSLTSINGKQFEKVPDSSLEFLILASDGLWDDVVSNEEAVGMI-KAIEDP--- 330
352 TREGKSAADARVEAACNRLANKAVQRGSDNVTVMVVRI 389
331 -----EAGAKLMEAVQRGSDNITCVVVR 356

RESULT 6
T08606
protein phosphatase 2C-like protein Spalten - slime mold (Dictyoetelium discoideum)
C:Species: Dictyoetelium discoideum
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C:Accession: T08606
R:Aubry, L.; Firtel, R.A.

submitted to the EMBL Data Library, August 1997
A:Reference number: Z16454
A:Accession: T08606
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-975 <AUB>
A:Cross-references: EMBL:AF019985; NID:g2425120; PID:g2425121
A:Experimental source: strain AX3
C:Genetics:
A:Gene: spnA

Query Match 18.2%; Score 368; DB 2; Length 975;
Best Local Similarity 29.1%; Pred. No. 7.2e-19;
Matches 118; Conservative 56; Mismatches 152; Indels 80; Gaps 17;

QY 8 PEPERSRPAAGKEAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGSGSLATSIS 67
DB 620 PKPPKPKPI--KEPKKPVK-ESKPKKE-----PKPIKPKESKEPKEP 661
QY 68 QMVKTEGKGAKRTS-----EEKNGSEEL-----VEKKVKCASSVIFGLKGYVAERKE 117
DB 662 KEPKPTKPKKETSQVDAAESKNGADSCGNGVGSKIKLESQ--FG-----SLQGR 713
QY 118 REEMQDAHVILNDITEECR---PPSSILTRVSYPAVFDGHHGIRASKFAAQNHLHQNLI-- 172
DB 714 RKNMEDTHVILNLMGAVTYANGPPKDI--PISYAVAYDGHGGTGTSTLTLEPTVHNCVLNS 771
QY 173 RKFPKGDVISVETKVRCLDTFKHTDEFLKQASSQKPAWKDGGTATCVLAVDNILYIA 232
DB 772 QSFDRGD-----YEQAFRDAYAEADIVIEKCE-----KSGSTGVSAALLVGNKLYTA 818
QY 233 NLGDSRAILCRVNEESQKHAALS-----LSKEHNPTQYERMRIOKAGNVDRDGRVLGV 287
DB 819 NVGDSEIVLARAQPNANPKGPVTFYEVLLSYKHLASDDQEKVKRVTDLGGMIIFNELFGSL 878
QY 288 EYSRSIGDGQYKRCGTVSPDIRCQLTNDRILLACDGLFKVFTPEEAVNFIL 342
DB 879 AVSRSGDKKEYKEGKKFC--VSDPVQVTTDLTARDHFFILACDGLWDDVVEAVQVFV- 935
QY 343 SCLEDEKIQTRGKSAADARVEAACNRLANKAVQRGSDNVTVMVV 388
DB 936 -----QRNIKLGKATE-----ISELLAQSDYDRGSGDNITVIV 970

RESULT 7
T52337
phosphoprotein phosphatase (EC 3.1.3.16) 2C [imported] - common ice plant
C:Species: Mesembryanthemum crystallinum (common ice plant)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 01-Mar-2002
C:Accession: T52337
R:Miyazaki, S.; Koga, R.; Bohner, H.J.; Fukuhara, T.
Mol. Gen. Genet. 261, 307-316, 1999
A:Title: Tissue- and environmental response-specific expression of 10 PP2C transcripts
A:Reference number: Z26045; MUID:99200489; PMID:10102366
A:Accession: T52337
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <MIY>
A:Cross-references: EMBL:AF075580; PIDN:AAC36698.1
C:Genetics:
A:Gene: PP2C
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220
C:Keywords: phosphoric monoester hydrolase

Query Match 18.1%; Score 365; DB 2; Length 359;
Best Local Similarity 31.8%; Pred. No. 3.1e-19;
Matches 92; Conservative 59; Mismatches 94; Indels 44; Gaps 10;

QY 116 GEREEMQDAHVILNDITEE-----CRPPSSILTRVSYPAVFDGHHGIRASKFAAQNHLHQ 169
DB 58 GPKYMEDESHIRDDLSVQLGSLFRCPKPS-----AFYGVFDGHHGSEAAAYVRENVMR 111
QY 170 NLIR--KFPKG---DVISVETKVRCLDTFKHTDEFLKQASSQKPAWKDGGTATCVLA 224

Db 112 PFDVSPFEASELDEIFUE-GVENCRLRAFFLAD---LALADDCSISTSGTALTALV 167
Qy 225 VDNILYIANLGSRAILCRYNESOKHAALSKEHNPTQYEEERMRIQKAGNVRDGRVL 284
Db 168 LGRLLIVANAGDCRAVLCKGE-----AIDNSQDHRFPTYPEKRVVEELGGYVDDGYLN 221
Qy 285 GVLEVSRTSGDQYK-----RCGVTSVPDIRCQLTNDPDRFILLACDGLFKVFTPEEAVN 339
Db 222 GVLVSRAIGDMKLPKGSAPLISEPELRQIILTEDDEFLLIGCDGIWDVSSQAVS 281
Qy 340 FILSCLEDEKIOTREGSKAADARYAACNRLANKAVQSGADNVTVMVV 388
Db 282 IV-----RWGLKRHDDP-QSAKDLVNEALRRHTDNLTLIV 318
RESULT 8
T50783
protein phosphatase 2C-like protein - Arabidopsis thaliana
N:Alternate names: protein T30N20.10
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Jun-2001
C:Accession: T50783
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirksee, W.; Stiekema, W.; Bancroft, I.; Mew
submitted to the Protein Sequence Database, July 2000
A:Reference number: Z25240
A:Accession: T50783
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-348 <BEV>
A:Cross-references: EMBL:AL365234
A:Experimental source: cultivar Columbia; BAC clone T30N20
C:Genetics:
A:Map position: 5
A:Introns: 27/2; 70/1; 103/1; 156/1; 185/1; 209/3; 234/3
A:Note: T30N20.10
C:Superfamily: human phosphoprotein phosphatase 1A
Query Match 18.1%; Score 364.5; DB 2; Length 348;
Best Local Similarity 36.4%; Pred. No. 3.2e-19;
Matches 103; Conservative 47; Mismatches 86; Indels 47; Gaps 13;
Qy 109 GYVAERKGEREEMQD-AHVILNDITECPSPSLITRVSYFAVFDGHHGIRASKFAQNL 167
Db 35 GY-ASSAGKRSSNEDFFETRIDGNGEI-----VGLFGVFDGHHGARAAYVKRHL 84
Qy 168 HQNLIRKPKGDVISVEKTVKRCCLDTFKHTDEEFLKQASSQKPAWKD-GSTATCVLAVD 226
Db 85 FSNLI-THPK--FIS--DTKSAITDAYNHTDSSELLKSENHN--RDAGSTASTAILVG 135
Qy 227 NILYIANLGSRAILCRYNESOKHAALSKEHNPTQYEEERMRIQKAGNVRDGRVLGV 286
Db 136 DRUVANVAGDSRAVIRSGGK-----AIAVSRDHKPDQSDERERENAGGFV---MWAGV 186
Qy 287 LEVSRSIGDQYKRCGVTSVPDIRCQLTNDPDRFILLACDGLFKVFTPEEAVNFILSCLE 346
Db 187 LAVSRAFGORLLKQY-VVADPEIQEBKIDCTLEFLIASDGLWDFVSEAAVAVV----- 240
Qy 347 DEKIOTREGSKAADARYAACNRLANKAVQSGADNVTVMVV 389
Db 241 -----KEVEDP--EDSAKLVGGAIKRGSADNITCVVVR 272
RESULT 9
H96700
protein F12A21.5 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H96700
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H96700
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <STO>
A:Cross-references: GB:AE005173; NID:gl1072032; PIDN:AAG28911.1; GSPDB:GN00141
C:Genetics:
A:Gene: F12A21.5
A:Map position: 1
Query Match 17.9%; Score 362; DB 2; Length 464;
Best Local Similarity 29.3%; Pred. No. 7.3e-19;
Matches 108; Conservative 59; Mismatches 104; Indels 98; Gaps 13;
Qy 102 SVIFGLKGY-VARKEGEREEMQDAHVILNDITECPSPSLITRVSYFAVFDGHHGIRAS 160
Db 113 TVSFGGNGFGWGRNGKKFMEDTHRIV-----PCLVGNS---KGSFFGVYDGHGAKAA 164
Qy 161 KPAQNHLQNLIRKFP--KGDVISVEKTVKRCCLDTFKHTDEEFLKQASSQKPAWKDGT 218
Db 165 EFVAENLHYVEMENCKGEEKVE-----AFKAAFLRTDRDLEFKVTKESQLKGVVSG 219
Qy 219 ATCVLAV--DNILYIANLGSRAILCRYNESOKHAALSKEHNPTQYEEERMRIQK--- 273
Db 220 ACCVTAVIQDEMIVSNLGCRAVLCRAG-----VAEALTDDEKFCRDEKERISQSL 273
Qy 274 -----AGGNVRD---GRVLGVLEVSRSIGDQYKRCGVTSVPDIRCQLTNDPDRFI 321
Db 274 IPFWTFLQGGYVDNHQGAWRVQGVILAVRSIGDAHLKK-WVVAEPETRVLELEQDMEFL 332
Qy 322 LLACDGLFKVFTPEEAVNFILSCLE-----EBEKIQ-----TREG 355
Db 333 VLASDGLWDFVSNQEAAYTVLHVAOKRTPKESEENLVQGFVNMSPSSKLRLASLVKSP 392
Qy 356 KSAADARY-----EAAACNRLANKAVQSGADNV 383
Db 393 RKAQSQSYNNSESPSLNREIGSFSPKSPITFWKSLMAKAAACKELANLAKRGSMDI 452
Qy 384 TVMVVRIGH 392
Db 453 TVVIIDLNH 461
RESULT 10
T45778
protein phosphatase 2C-like protein - Arabidopsis thaliana
N:Alternate names: protein F26013.110
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 03-Jun-2002
C:Accession: T45778
R:Delaney, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23013
A:Accession: T45778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-361
A:Cross-references: EMBL:AL133452
A:Experimental source: cultivar Columbia; BAC clone F26013
C:Genetics:
A:Map position: 3
A:Introns: 49/3; 108/3
A:Note: F26013.110
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220
Query Match 17.8%; Score 358.5; DB 2; Length 361;
Best Local Similarity 30.6%; Pred. No. 9.4e-19;

QY 381 -----DNTVMVVR 389
 ||:|:|:
 Db 315 TGECDNMTILVQ 328

 RESULT 12
 T04263
 phosphoprotein phosphatase (EC 3.1.3.16) AB11 - Arabidopsis thaliana
 N:Alternate names: protein F20B18.190
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999
 R:Accession: T04263; A54588
 R:By:Van, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hohseisel, J.; Mewes, H.W.; Mayer, K.F.
 submitted to the Protein Sequence Database, March 1999
 A:Reference number: Z15263
 A:Accession: T04263
 A:Molecule type: DNA
 A:Residues: 1-434 <BEV>
 A:Cross-references: EMBL:AL049483
 A:Experimental source: cultivar Columbia; BAC clone F20B18
 R:Meyer, K.; Leube, M.P.; Grill, E.
 Science 264, 1452-1455, 1994
 A:Title: A protein phosphatase 2C involved in ABA signal transduction in Arabidopsis th
 A:Reference number: A54588; MUID:94255767; PMID:8197457
 A:Accession: A54588
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-104, V', 106-434 <MEY>
 A:Cross-references: GB: X78886; NID: G509418; PIDN: CAA55484.1; PID: G509419
 C:Genetics:
 A:Gene: AB11
 A:Map position: 4
 A:Introns: 183/3; 280/3; 316/1
 A:Note: F20B18.190
 C:Keywords: phosphoric monoester hydrolase

```

Query Match      17.5%; Score 352.5; DB 2; Length 434;
Best Local Similarity 29.4%; Pred. No. 3.3e-18;
Matches 125; Conservative 65; Mismatches 148; Indels 87; Gaps 19;

QY      2 DLFGDLPEPER-SPRPAACKGKGLLLFDDLPASPSTDSGGGPLELFDLPASSGD-- 58
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
          45 DLWVSLFETSSCVSGHSGHSEKRVILSRINSLNKNKESAAADIVVVD---ISAGDEI 100

Db

```

Db	101	NGSDITSEKXMIKRTB	-----SRSLFEFK-----SVPLYGFTSIC-----GR	137
Qy	118	REEMODAHVILNDITECPSPSLI	-----TRVSYFAVFDGHGIGIRASKPAQNLHQ	169
Db	138	REMEDA---VSTIPREFLOSSGMLDGRFPDQSAAHF	FGVYDGHGSGSVANYCREMHIL	194
Qy	170	NLIRKPPK-----GDVISVEKTVKRCILDTFKHT	DEEFLKQASSQKPAWKDGSTATCV	222
Db	195	ALAEETIAKEKPMLCDGDT-WLEKW-KKALFN	SFLRVDSEIESVAPETV-----GSTSWA	247
Qy	223	LAVDNILYITANLGDRAILCRYNEBQKHAALSLSKEHNPTQYEE	RMRIOKAGNV---R	279
Db	248	VFPSPSHIFVANGDSRAVLGR	-----GKTALPLSDVHDKEDREDEAARIEAAGGKVLQWN	301
Qy	280	DGRVLGVLEVSRSIGDQYKRCQVTSVPDIRRCQLTENDR	FILLACDGLFKVFTPEZAVN	339
Db	302	GARVFGVLAMSRSIGD-RYLKPSII	PDPEVTAVKRVKEDDCLILASDGVWDVMTDEACE	360
Qy	340	FI-----LSCLEDEKIOTREGKSAADARYEAACN	LANKAVORGSDNV	383
Db	361	MARKRILLWHKKNAVAGDASLTLADER--RKEGK---	DPAAMSAEYLSUKIAIORGSKDNI	415
Qy	384	TVMV	388	
Db	416	SVVVV	420	

RESULT 13

F84650
probable protein phosphatase 2C [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 01-Mar-2002
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84650
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-392 <STO>
A:Cross-references: GB:AE002093; NID:g4874313; PIDN:AAD31375.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g25620
A:Map position: 2
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220

Query Match 17.4%; Score 352; DB 2; Length 392;
Best Local Similarity 27.8%; Pred. No. 3.1e-18;
Matches 110; Conservative 73; Mismatches 152; Indels 60; Gaps 13;
QY 7 LPERSPRPAGKEAQKGLFLDLPASSTDSGGGLFLDLPASSGDSGLATSI 66
DB 7 TSDPENGSSYGGK--PNNLSF-----SSSAAAAYVQTFDGERSLAPCNKSLVRH- 58
QY 67 SOMVTEGKAKRTS-BEEKNGSELVEKKVKKASSVIFLKGVAERKGEREMODAH 125
DB 59 SSLVKTMTSDISVENEFTIEKNKSEFPATRSAGMSDI-----GSRSSMEDAY 106
QY 126 VLNDITETCPSPSLITRVSPVAFDGGGIRASKFAQNLHQLI--RKFPKGDVTSV 183
DB 107 LCVDFMDSFGLNLSEAGSFAYFVDFGGHGAABFACHIPRYTIVEDQEPF----- 159
QY 184 EKTVCRLDTPKHTDEEFLKQASQKPAWKDGTATCVLAVDNLILYANLGDRAILCR 243
DB 160 -SEINKVLSAFLQDTAFLEACSLDGLASGTTALAAIFGLSLVVAAGDCRAVLSR 217
QY 244 YNESQKHAALSLSKEHNPTQYERMRIOKAGNVDRGRVLGVLEVSISGD----QQYK 299
DB 218 QGK-----ATMSRDHKPMSSKERRIEASGSHVFDGVLNGLNVAALGDFHEGKK 271
QY 300 R-----CG-VTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTR 353
DB 272 KKGSDCGPLIAEPELMTTKLTEDEFLIIGCDGVDFVMSQNAVDFARRLQSHNDPVM 331
QY 354 EGKSAADARYEACNPLANKAVQGSADNVTVMVV 388
DB 332 CSK-----ELVEEALKRKSSADNVTVAVV 354

RESULT 14

T00750
probable protein phosphatase 2C [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T20B5.6
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL Data Library, November 1997
A:Description: Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence.
A:Reference number: Z14159
A:Accession: T00750
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-404 <ROU>
A:Cross-references: EMBL:AC002409; NID:g2623294; PID:g2623300
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84834
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-404 <STO>
A:Cross-references: GB:AE002093; NID:g2623300; PIDN:AAB86446.1; GSPDB:GN00139
C:Genetics:
A:Gene: T20B5.6; At2g40860
A:Map position: 2
A:Introns: 178/1; 200/2; 273/3; 308/3; 340/3

Query Match 17.4%; Score 351; DB 2; Length 404;
Best Local Similarity 29.3%; Pred. No. 3.9e-18;
Matches 110; Conservative 56; Mismatches 117; Indels 92; Gaps 13;
QY 65 SISQVMTKTEGK---AKRTTSEENKNGSE-----ELVEKKVKKASSV 103
DB 59 SIWEQVRGKQGHLEKTSNSQSDTDGADIINKSGDYRDTVNVWFSGECLSKK--SSVST 116
QY 104 IFGLKCYVAERK-----GEEEMQDAHVILNDITEECRPPSSLITRVS 146
DB 117 VFDVKLWSSSTDEPSRYVPVISCGFATCGRESMEDTHFIIPMCNE-----ESIH 168
QY 147 YFAVFDGCHGIRASKFAQNLHQLIRPKPGDVTISVEKT-VKRCILDTFKHTDEEFLKQ 205
DB 169 LFAIPFGHGAARAAFSQVL-----PGLVQSLCSTSAGEALSQAFTVDLAFROE 219
QY 206 ASSQKPA-----WKDGSATATCVLAVDNLILYANLGDRAILCRYNESQKHAALSLSK 258
DB 220 LDSHRQKRVSKQKWHFPGCTATASLLVENKLFVANVGDSRAILCRAGH-----PFALSK 273
QY 259 EHNPTQYERMRIOKAGNVN---DGRVLGV-LEVSRSIGDGQYKRCQVTSVPDIRRQ 313
DB 274 AHLATCIDERNRVIGEGRIEVLVDTWRVAPAGLQVTRSIGDDDLKP-AVTAEPSEISETI 332
QY 314 LTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAADARYEACNPLANK 373
DB 333 LSADDFLVNASDGLVMDVNDSEVIGIIRDTVKPESMCKS-----RLATE 377
QY 374 AVQGSADNVTVMVV 388
DB 378 AAARGSGDNITVIVV 392

RESULT 15

T06308
protein phosphatase 2C homolog F11C18.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 15-Jun-2001
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De
ewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15589
A:Accession: T06308
A:Molecule type: DNA
A:Residues: 1-357 <BEV>
A:Cross-references: EMBL:AL049607; GSPDB:GN00062; ATSP:F11C18.60
A:Experimental source: cultivar Columbia; BAC clone F11C18
C:Genetics:
A:Gene: ATSP:F11C18.60
A:Map position: 4
A:Introns: 39/3; 61/1; 97/2; 148/3; 190/3; 232/1; 257/3; 275/2; 293/3
C:Superfamily: human phosphoprotein phosphatase 1A

Query Match 17.3%; Score 350; DB 2; Length 357;
Best Local Similarity 28.5%; Pred. No. 3.9e-18;
Matches 95; Conservative 59; Mismatches 95; Indels 84; Gaps 11;

QY 111 VAERKGEREMQDAHVILNDITEECRPPSSLITRVSYFAVEDGGHGGIRASKFAAQNLHQN 170
Db 26 LSSMQGWRASMEDAAAILDLDD-----NTSFLGVYDGGHGGKVSFKFCAYLHQ 75
QY 171 LI--RKFPKGDV-ISVEKTVKRCILDTFKHTDEEFLKQA----- 206
Db 76 VLSDEAVAAGDVGTSLQKAFR--MDEMKGQGRWRELAVLGDKINKFSGMIEGLIWSPR 133
QY 207 ---SSQKP-AW-----KQGSTATCVLAVDNILYIANLGDSTRAILCRVNEESQ 249
Db 134 SGDSANKPDAWAPEEGPHSDPAGNSGSTACVAVVRDKQLFVANAGDSRCVI-----SR 187
QY 250 KHAALSLSKEHNPTQYEEHRIQKAGNVDRDGRVLGVLEVSRSIGDQYKRCG----- 302
Db 188 KNQAYNLSRDHKPDLEAEKERILKAGGFIHAGRVNGSLNLSRAIGDMETKQKFLPSEKQ 247
QY 303 -VTSVPDIRRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDESKIQTREGKSAADA 361
Db 248 IVTASPDVNTVELCDDDFLVLACDGIWDCMTSQQLVDFIHEQLNSE-----T 295
QY 362 RYEAACNRLANKAVORGA-----DNVTVMVVR 389
Db 296 KLSVVCEKVLDRCLAPNTSGEGCDNMTILVR 328

Search completed: April 12, 2004, 09:07:15
Job time : 22 secs

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:01:42 ; Search time 17 Seconds
(without alignments)
1200.677 Million cell updates/sec

Title: US-09-935-124A-2
Perfect score: 2018
Sequence: 1 MDLFGDLPBPSRPAAGK.....KAVQGSADNTVMVVRIGH 392

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	401.5	19.9	300	1 P2C PARTE	P49444 paramemium
2	370.5	18.4	414	1 P2C3 SCHPO	Q09173 schizosacch
3	366.5	18.2	454	1 FEM2 HUMAN	P49593 homo sapien
4	352.5	17.5	434	1 P2C1 ARATH	P49597 arabidopsis
5	348	17.2	370	1 P2C2 SCHPO	Q09172 schizosacch
6	347	17.2	356	1 P2C2 CAEEL	P49596 caenorhabdi
7	342	16.9	382	1 P2CA BOVIN	O62829 bos taurus
8	341.5	16.9	450	1 FEM2 RAT	O9WV77 rattus norv
9	340	16.8	382	1 P2CA RABIT	P35814 cryptolagus
10	340	16.8	382	1 P2CA RAT	P20650 rattus norv
11	338	16.7	382	1 P2CA MOUSE	P49443 mus musculu
12	336	16.7	382	1 P2CA HUMAN	P35813 homo sapien
13	333	16.5	423	1 P2C2 ARATH	O04719 arabidopsis
14	326	16.2	390	1 P2CB MOUSE	P36993 mus musculu
15	319	15.8	390	1 P2CB RAT	P35815 rattus norv
16	317.5	15.7	281	1 P2C1 YEAST	P35182 saccharomyc
17	314	15.6	387	1 P2CB BOVIN	O62830 bos taurus
18	313	15.5	479	1 P2CB HUMAN	O75688 homo sapien
19	306	15.2	347	1 P2C1 SCHPO	P40371 schizosacch
20	305.5	15.1	464	1 P2C2 YEAST	P39966 saccharomyc
21	305	15.1	388	1 P2C3 ARATH	P49599 arabidopsis
22	300	14.9	491	1 P2C1 CAEEL	P49595 caenorhabdi
23	289	14.3	468	1 P2C3 YEAST	P34221 saccharomyc
24	282.5	14.0	399	1 P2C4 ARATH	P49598 arabidopsis
25	271.5	13.5	405	1 P2C1 LEICH	P36982 leishmania
26	269.5	13.4	542	1 P2C3 MOUSE	O61074 mus musculu
27	267.5	13.3	393	1 P2C4 YEAST	P38089 saccharomyc
28	264	13.1	449	1 FEM2 CAEEL	P49594 caenorhabdi
29	256.5	12.7	543	1 P2CG BOVIN	P79126 bos taurus
30	255.5	12.7	546	1 P2CG HUMAN	O15355 homo sapien
31	211.5	10.5	2493	1 CYAA USTMA	P49606 ustilago ma
32	211	10.5	605	1 P2CD HUMAN	O15237 homo sapien
33	209	10.4	538	1 PDP1 BOVIN	P35816 bos taurus

34	209	10.4	598	1 P2CD MOUSE	Q9qz67 mus musculu
35	208	10.3	2300	1 CYAA_NEUCR	O01631 neurospora
36	207	10.3	538	1 PDP1 RAT	O88483 rattus norv
37	206	10.2	1839	1 CYAA_SACKL	P23466 saccharomyc
38	204.5	10.1	383	1 P2C4 SCHPO	O14156 schizosacch
39	203	10.1	538	1 PDP1 HUMAN	Q9p0j1 homo sapien
40	202	10.0	581	1 KAPP_ARATH	P46014 arabidopsis
41	194	9.6	529	1 PDP2 HUMAN	Q9p2j9 homo sapien
42	188	9.3	530	1 PDP2 RAT	O88484 rattus norv
43	185.5	9.2	2026	1 CYAA_YEAST	P08678 saccharomyc
44	178	8.8	504	1 TAB1 HUMAN	Q15750 homo sapien
45	178	8.8	2145	1 CYAA_PODAN	Q01513 podospora a

ALIGNMENTS

RESULT 1

ID	P2C PARTE	STANDARD;	PRT;	300 AA.
AC	P49444;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Protein phosphatase 2C (EC 3.1.3.16) (PP2C).			
OS	Paramemium tetraurelia.			
OC	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;			
OC	Paramemium.			
OX	NCBI_TaxID=5888;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	STRAIN=Stock 51;			
RC	MEDLINE=95105156; PubMed=7806499;			
RA	Klump S., Hanke C., Donella-Deana A., Beyer A., Kellner R.,			
RA	Pinna L.A., Schultz J.E.;			
RT	"A membrane-bound protein phosphatase type 2C from Paramemium			
RT	tetraurelia. Purification, characterization, and cloning."			
RL	J. Biol. Chem. 269:32774-32780(1994).			
CC	- FUNCTION: Enzyme with a broad specificity.			
CC	- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +			
CC	phosphate.			
CC	- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).			
CC	- SUBCELLULAR LOCATION: Membrane-bound.			
CC	- PTM: The N-terminus is blocked.			
CC	- SIMILARITY: Belongs to the PP2C family.			

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC	EMBL; Z36985; CAA85448.1; --
DR	PIR; A55804; A55804.
DR	HSSP; P35813; LAQG.
DR	InterPro; IPR001932; PP2C-like.
DR	InterPro; IPR000222; PP2C.
DR	Pfam; PF00481; PP2C; 1.
DR	SMART; SM00331; PP2C SIG; 1.
DR	SMART; SM00332; PP2C; 1.
DR	PROSITE; PS01032; PP2C; 1.
FW	Hydrolase; Magnesium; Manganese; Membrane.
FT	METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT	METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT	METAL 57 57 MANGANESE 1 AND 2 (BY SIMILARITY).
FT	METAL 237 237 MANGANESE 2 (BY SIMILARITY).
FT	METAL 289 289 MANGANESE 2 (BY SIMILARITY).
SQ	SEQUENCE 300 AA; 33739 MW; BC0318B4FF7724EC CRC64;

Query Match 19.9%; Score 401.5; DB 1; Length 300;
Best Local Similarity 33.0%; Pred. No. 7.7e-22;

FEM2 HUMAN
ID FEM2 HUMAN STANDARD; PRT; 454 AA.
AC P49593; Q36PW2;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ca(2+)/calmodulin-dependent protein kinase phosphatase (EC 3.1.3.16)
DE (Cam-kinase phosphatase) (CamKpase) (Partner of PIX 2) (hFEM-2)
DE (Protein phosphatase 1F)
DE (Protein phosphatase 1F)
GN PPM1P OR POPX2 OR KIAA0015.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21570215; PubMed=11559703;
RA Tan K.M.L., Chan S.L., Tan K.O., Yu V.C.;
RT "The Caenorhabditis elegans sex-determining protein fem-2 and its
human homologues, hFEM-2, are Ca2+/calmodulin-dependent protein kinase
phosphatases that promote apoptosis.";
RL J. Biol. Chem. 276:44193-44202(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21853182; PubMed=11864573;
RA Koh C.G., Tan E.J., Manser E., Lim L.;
RT "The p21-activated kinase PAK is negatively regulated by POPX1 and
POPX2, a pair of serine/threonine phosphatases of the PP2C family.";
RL Curr. Biol. 12:317-321(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96051387; PubMed=7584026;
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. I.
The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
analysis of randomly sampled cDNA clones from human immature myeloid
cell line KG-1.";
RL DNA Res. 1:27-35(1994).
CC -!- FUNCTION: Dephosphorylates and concomitantly deactivates Cam-
kinase II activated upon autophosphorylation, and Cam-kinases IV
and I activated upon phosphorylation by Cam-kinase kinase.
CC Promotes apoptosis.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
CC -!- SUBUNIT: Associates with F1Aalpha.
CC -!- SIMILARITY: Belongs to the PP2C family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
or send an email to license@ebi.ac.uk).
CC
CC EMBL; AF305840; AAL15579.1; -;
CC DR EMBL; AF520615; AAM76059.1; -;
CC DR EMBL; D13640; BAA02803.1; -;
CC DR Genew; HGNC:19388; PPM1F;
CC DR InterPro; IPR001932; PP2C-like.
CC DR InterPro; IPR000222; PP2C.
CC DR Pfam; PF00481; PP2C; 1.
CC DR SMART; SM00331; PP2C_SIG; 1.
CC DR SMART; SM00332; PP2C; 1.
CC DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Apoptosis; Multigene family.
FT DOVAIN 101 107 POLY-GLU.
FT METAL 360 360 MANGANESE 2 (BY SIMILARITY).
FT METAL 404 404 MANGANESE 2 (BY SIMILARITY).
FT CONFLICT 202 202 G -> D (IN REF. 1).

SQ SEQUENCE 454 AA; 49830 MW; 2B49262333D4C9CF CRC64;
Query Match 18.2%; Score 366.5; DB 1; Length 454;
Best Local Similarity 28.3%; Pred. No. 4.5e-19;
Matches 127; Conservative 65; Mismatches 145; Indels 111; Gaps 16;
QY 10 PERSRPPAAGKAQKGPL--LFDDLPASSTDSGGPGLLFDLPASSGD-----SG 60
DB 6 PQKSPMASGAETPGFLDTLLQDPALLNPE-----DPLFWKAGTVLSQEEVEG 56
QY 61 SLA-----TSISQMVKTE-----GKAKAKTSEKXNGSEELVE 94
DB 57 ELAELAMGFLGSRKAPPPLAALAHEAVSQLLQTLSEFRKLPRREEEEDDEEEKAP 116
QY 95 KKVCKASSVIFGLKGVVAERKGE-----REEMQDAHVIL 128
DB 117 VTLLDAQSLAQFFNRLMEVAGQWQKQVPLAARASQOWLSVHAIKNTRRKMDRHVSL 176
QY 129 NDITECRPPSLITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRK-----PPKGDVISV 183
DB 177 PSF-NQLFGLSDPVNR-AYFAVFDGHHGVDAAARYAAHVHTNAARQPELPTPEG----- 229
QY 184 EKTVRKCLLDTPKHTDEEFLKOASSQKPAWKGSTATCVLAVDNILYIANLGDSRAILCR 243
DB 230 -----ALREAFRTDQWFLKAKRER--LQSGTTGVGCALIAAGATLHVAVLGDQSQVILV- 280
QY 244 YNEESQKHAALSLSKEHNPTQYERVRKQKAGNVRD---GRVLGVLEVSRSIGDQVYKR 300
DB 281 -----QQGQWVKLMEPHPRQDEKARIEALGGFVSHMDCEWVNGTFLAVSRAIGD-VFOK 334
QY 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVTPPEANVNFILSCLEDEKIQTRREGSAAD 360
DB 335 PYVSGEADAASRALTGSEDIYLLACDGFDDVVFHQEVVGLVQSHL-----TRQQSGUR 388
QY 361 ARYEAACNELANKAVORGSAADNTVMVW 388
DB 389 VAE-----LVAAERGRSHDNITVMVW 411
RESULT 4
P2C1_ARATH STANDARD; PRT; 434 AA.
ID P2C1_ARATH STANDARD; PRT; 434 AA.
AC P49597; Q43717; Q94C87;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Protein phosphatase 2C ABI1 (EC 3.1.3.16) (PP2C) (Absciscic acid-
insensitive 1).
GN ABI1 OR AT4G26080 OR F20B18.190.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT ASP-180.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=94255767; PubMed=8197457;
RA Meyer K., Leube M.P., Grill E.;
RT "A protein phosphatase 2C involved in ABA signal transduction in
Arabidopsis thaliana.";
RL Science 264:1452-1455(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Leaf;
RX MEDLINE=95007758; PubMed=7923358;
RA Mindrinos M., Katagiri F., Yu G.L., Ausubel F.M.;
RT "The A. thaliana disease resistance gene RP2 encodes a protein
containing a nucleotide-binding site and leucine-rich repeats.";
RL Cell 78:1089-1099(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Leaf;

RA	Medline=94255766; PubMed=7910981;	RT	genome."
RA	Leung J., Bouvier-Durand M., Morris P.C., Guerrier D., Cheifor F.,	RL	Science 302:842-846(2003).
RA	Girardat J.,	CC	!- FUNCTION: Involved in abscisic acid (ABA) signaling pathway.
RA	"Arabidopsis ABA response gene AB11: features of a calcium-modulated	CC	!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
RT	protein phosphatase."	CC	phosphate.
RL	Science 264:1448-1452(1994).	CC	!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
RN	[4]	CC	!- SIMILARITY: Belongs to the PP2C family.
RP	SEQUENCE FROM N.A.	CC	
RC	STRAIN=sv. Columbia;	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
RX	MEDLINE=20083488; PubMed=10617198;	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
RA	Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,	CC	the European Bioinformatics Institute. There are no restrictions on its
RA	Pohl T., Duesterhoeft A., Stickema W., Entian K.-D., Terryn N.,	CC	use by non-profit institutions as long as its content is in no way
RA	Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,	CC	modified and this statement is not removed. Usage by and for commercial
RA	Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller T.,	CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/
RA	Kreis M., Delserny M., Puigdomenech P., Watson M., Schmidtheini T.,	CC	or send an email to license@isb-sib.ch).
RA	Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,	CC	
RA	Vos P., Heiseisel J., Zimmermann W., Wedler H., Ridley P.,	DR	EMBL; X78886; CAAS5484.1; -
RA	Langham S.-A., McCullagh B., Billham L., Robben J.,	DR	EMBL; U12856; AAS50237.1; -
RA	Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,	DR	EMBL; X77116; CAAS4383.1; -
RA	Braeken M., Weltjens I., Voet M., Baetiaens Y., Aert R., Defoor E.,	DR	EMBL; AL049483; CAB39673.1; -
RA	Weitzenecker T., Boche G., Ransperger U., Hilbert H., Braun M.,	DR	EMBL; AL161564; CAB79463.1; -
RA	Holzer E., Brandt A., Peters S., van Staveren W., Dirkse W.,	DR	EMBL; AY035073; AKS59578.1; -
RA	Moeljan P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,	DR	FIR; T04263; T04263.
RA	Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,	DR	HSSP; P35813; LA60.
RA	De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,	DR	InterPro: IPR002048; EF-hand.
RA	Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,	DR	InterPro: IPR001932; PP2C-like.
RA	Clark L., Doggett J., Hall S., Kay M., Lennard N., McRay K., Mayes R.,	DR	InterPro: IPR000222; PP2C.
RA	Pettett A., Rajadream M.A., Lyne M., Benes V., Rechmann S.,	DR	Efam; PF00481; PP2C; 1.
RA	Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,	DR	SMART; SM00331; PP2C SIG; 1.
RA	Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,	DR	SMART; SM00332; PP2CG; 1.
RA	Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,	DR	PROSITE; PS00018; EF HAND; 1.
RA	Neumann S., Argirion A., Vitale D., Liguori R., Piravandi E.,	DR	PROSITE; PS01032; PP2C; 1.
RA	Masenet O., Quigley F., Clabaud G., Wuendlein A., Felber R.,	KW	Hydrolase; Magnesium; Manganese; Multigene family; Calcium-binding.
RA	Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,	FT	CA BIND 93 104
RA	Cheford F., Cooke R., Berger C., Monfort M., Casacuberta E.,	FT	DOMAIN 417 420
RA	Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,	FT	VARIANT 180 180
RA	Perez-Perez A., Furnelle B., Bent E., Johnson S., Tacón D., Jesse T.,	FT	POLY-VAL.
RA	Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,	FT	G -> D (WILTY PHENOTYPE AND ABA-
RA	Frisman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,	FT	INSENSITIVE SEED GERMINATION AND GROWTH).
RA	Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,	FT	G -> R (IN REF. 5).
RA	Parnell L., Dedhia N., Gnoj L., Schutz K., Huang B., Spiegel L.,	FT	I -> V (IN REF. 1).
RA	Sekton M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,	FT	CONFLICT 24 24
RA	Stonking T., Kalicki J., Graves T., Harmon G., Edwards J.,	FT	CONFLICT 105 105
RA	Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,	FT	SEQUENCE 434 AA; 47505 MW; 4A4CS4F0419SF572 CRC64;
RA	Mix P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,	QY	2 DLFGLPEPER-SPRPAAGKEAQKGLPLFDLPPASSTDSGGGLLFDLPPASGD-- 58
RA	Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,	Db	45 DLMVSLPETSSCSVSGSHGSEKVLISRINSPNLNKKESAADIWVVD-----ISAGDEI 100
RA	Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,	QY	59 SGLSATSISQMV-KTEGKAGAKTSEEEKNGSEELVEKKVKYASSVIFGLKGYVAERKGE 117
RA	Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,	Db	101 NGSDITSEKMKISRT------SRSLFEFK-----SVPLYGFTSIC-----GR 137
RA	Antonou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,	QY	118 REEMQDAHVILNDITEECRPPSLI-----TRVSVFAVFDGHHGRASFAAQNHLQ 169
RA	Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,	Db	138 RPAMEDA---VSTIPFLSSGSMLDGRFDQSAHFFGVVDGSGSVQVANYCRMH 194
RA	Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,	QY	170 NLIRKPKK-----GDVISVETKVKRCLLDITFKHTDEEFLKQASQKPAWKGDTATCV 222
RA	Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,	Db	195 ALAEETAKKPKMLCDGDT-WLEKW-KKALFNSFLRVDSESVAPETV-----GSTSVVA 247
RA	Chen E., Marra M.A., Martensen R., McCombie W.R.,	QY	223 LAVDNILYIANIGDSRAILCRYNSSQKHAALSLSKEHNPTQVEEMRITQKAGNV---R 279
RT	"Sequence and analysis of chromosome 4 of the plant Arabidopsis	Db	248 VVFPFHFVANGDSRAVLCR-----GKTALPLSDHDKPDRDEAARIEAAGGKIOWN 301
RT	thaliana."	QY	280 DGVILGVLESSIGGQVRCGVTSVPDIRCOLTPNDREFILLACDGLFKVFTPEAVN 339
RL	Nature 402:769-777(1999).	Db	302 GARVFGVLAWSRISIGD-RYLKPSIIPDPPEVAVKRVKDDCILASDGVDWMTDEACE 360
RN	[5]	QY	340 FI-----LSLCEDEKIQREKGAADARAEACNRLANKAVQGRSADNV 383
RP	SEQUENCE FROM N.A.	Db	361 MARKRILLWHKKNVAVAGDASLLADER--RKEGK---DPAAMSAAEVLKLAIQRGSKDNI 415
RC	STRAIN=sv. Columbia;		
RX	MEDLINE=22954850; PubMed=14593172;		
RA	Yamada K., Lim J.M., Chen H., Shinn P., Palm C.J.,		
RA	Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,		
RA	Karl-Neumann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,		
RA	Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,		
RA	Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,		
RA	Arakawa T., Barth J., Banno F., Bowser L., Brooks S.Y., Carninci P.,		
RA	Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,		
RA	Hayashizaki Y., Johnson-Hopson C., Hauan V.W., Iida K., Karnes M.,		
RA	Khan S., Koesena E., Ishida J., Jiang P.X., Jones T., Kawai J.,		
RA	Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,		
RA	Satou M., Tame S., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,		
RA	Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.,		
RT	"Empirical analysis of transcriptional activity in the Arabidopsis		

QY 384 TVMVV 388
Db 416 SVVVV 420

RESULT 5
P2C2_SCHPO STANDARD; PRT; 370 AA.
AC Q09172;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C homolog 2 (EC 3.1.3.16) (PP2C-2).
GN PTC2 OR SPCC1223.11.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RC MEDLINE=95163582; PubMed=7859738;
RX RA Shiozaki K., Russell P.;
RT "Counteractive roles of protein phosphatase 2C (PP2C) and a MAP
RL kinase homolog in the osmoregulation of fission yeast.";
RL EMBO J. 14:492-502(1995).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RC MEDLINE=21848401; PubMed=11859360;
RX RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Stewart A.,
RA Sgroves J., Peat N., Hayles J., Baker S., Baeham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squires A., Walsh S.V., Warren T., Whitehead S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Art R., Robben J., Gymonprez B.,
RA Weltjens I., Vanstreels E., Kieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RL "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: Has an important role in osmotic stability and cell
CC shape control. It may negatively regulate the osmosensing signal
CC transmitted through wsl map kinase.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the PP2C family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)
CC or send an email to license@isb-sib.ch.

CC EMBL; L34881; AAA67320.1; -.
DR EMBL; AL031579; CAA20880.1; -.
DR PIR; S54297; S54297.
DR HSSP; P35813; 1A6Q.
DR GeneDB SPombe; SPCC1223.11; -.
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C SIG; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Multigene family.
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 63 63 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 233 233 MANGANESE 2 (BY SIMILARITY).
FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
SQ SEQUENCE 370 AA; 40878 MW; DBDDB826F440AC50 CRC64;
Query Match 17.2%; Score 348; DB 1; Length 370;
Best Local Similarity 32.5%; Pred. No. 7.3e-18;
Matches 98; Conservative 47; Mismatches 103; Indels 54; Gaps 12;
QY 111 VAERKGEREEMQDAHVILNDITE--ECRPPSLITRVSYPVFDCHGIGIRASKFAAQNLIH 168
Db 26 VSHMQGWRISMEDAHCALLNFTDSNSNPPT-----SFFGVFDHGGDRVAKYCRQHL- 78
QY 169 QNLIRKFP---KGDVISVEKTVKRLDTEKHTDEEFLKQASSOKPAWKDGSTATCVLAV 225
Db 79 PDIIKQSQSFWKGN-----YDEALKSGFLAANALMQDRMQED--PSGCTATALLIV 129
QY 226 DN-ILYIANLGDRAILCRVNEESOKHAALSLSKEHNPTQYEERMRIOKAGENVDRGRLV 284
Db 130 DQOVLYCANAGDSRVILGR-----KGTAEPLSPDKPNNDVEKARITAAAGGFIIDFGRVN 183
QY 285 GYLEVSRSIGDQYKRCG-----VTSVPDIRCQLTPNDRFILLACDGLFKVFTPEE 336
Db 184 GSLALSRAIGDPEYKXSSLPPEKQIVTAFDVIHNDPDPDEFILACDGLWCKSSQQ 243
QY 337 AVNFILSCLEDEKIOTRGKGAADARYAACNLANKAVQRGS-----ADNVTVMVYRI 390
Db 244 VVEFV-----RRGIVARQS-LEVICENLMDRCIASNSCSCGICDNMTTICIVAF 291
QY 391 GH 392
Db 292 LH 293
RESULT 6
P2C2_CABEL STANDARD; PRT; 356 AA.
ID P2C2_CABEL
AC P49596;
DT 01-FEB-1996 (Rel. 33, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable protein phosphatase 2C T23F11.1 (EC 3.1.3.16) (PP2C).
GN T23F11.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC STRAIN=Bristol N2;
RA Swinburne J.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RN REVISIONS.
RA Durbin R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.

CC -1- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
CC -1- SIMILARITY: Belongs to the PP2C family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z46343; CA486456.2; --
CC PIR; T25181; T25181.
CC DR HSP; P35813; 1A6Q.
CC DR WormPep; T23F11.1; CE24009.
CC DR InterPro; IPR001932; PP2C-like.
CC DR InterPro; IPR000222; PP2C.
CC DR Pfam; PF00481; PP2C; 1.
CC DR SMART; SM00331; PP2C_SIG; 1.
CC DR SMART; SM00332; PP2C; 1.
CC DR PROSITE; PS01032; PP2C; 1.
CC DR PROSITE; PS01032; PP2C; 1.
CC KW Hypothetical protein; Hydrolase; Magnesium; Manganese.
CC FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
CC FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
CC FT METAL 59 59 MANGANESE 1 AND 2 (BY SIMILARITY).
CC FT METAL 228 228 MANGANESE 2 (BY SIMILARITY).
CC FT METAL 277 277 MANGANESE 2 (BY SIMILARITY).
CC SQ SEQUENCE 356 AA; 39064 MW; EDCB0841CFB026B5 CRC64;
CC -----
CC Query Match 17.2%; Score 347; DB 1; Length 356;
CC Best Local Similarity 31.4%; Pred. No. 8.2e-18;
CC Matches 101; Conservative 57; Mismatches 106; Indels 56; Gaps 12;
CC
CC QY 91 ELVEKKVKASSVIGLKGVAE---RKGEREMQDAHVILNDITECRPSSLIITVSY 147
CC DB 3 QTLSEPVTKESASCANENLYVGSSCQGVWRVDEDAHTLLSPDD-----PKCAF 54
CC
CC QY 148 FAVFDGHGGIRASKFAAONLHNL--RKFKPGDV-ISVEKTVKRLDTEKHTDEBFLK 204
CC DB 55 FAVFDGHGSKVSQVSGINLHKVVAQKEFEGNKEAIEKGFLE--LDQMRVDEETKD 112
CC QY 205 QASSQKPAWKDGSTATCVLAVDNILYIANLGDSRAILCRYNESQKHAALSLSKEHNPTQ 264
CC DB 113 DVS-----GTTAVVVLKEGDIYCGNAGDSRAVSSVSGE-----ARPLSPDHKPSH 158
CC QY 265 YERWRIQAGNVDRGRVLGVLEVSIGDQYKRCG-----VTSVPDIRRCQLTP 316
CC DB 159 ETEARRITAAAGGWFEFNRVNGNLALSRAIGDPAFKNCCTKPAEQIVTAFPDVITDKLTP 218
CC QY 317 NDRFILLACDGLFKVFTPEAVNFILSCLEDEKIQTRGKSNADARYEACNRLANKAV- 375
CC DB 219 DHEFIVLACDGIWDYMTNQEVVDFV-----RE-KLAEKDPQSCIEELLTRCLA 266
CC QY 376 ---QRG--SADNVTVWVRIGH 392
CC DB 267 PQCGVGLGCDNNTVVLGLLH 288
CC
CC RESULT 7
CC P2CA_BOVIN
CC ID_P2CA_BOVIN STANDARD; PRT; 382 AA.
CC AC O62829;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha).
CC GN PF01A.
CC OS Bos taurus (Bovine).
CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC OC Bovidae; Bovinae; Bos.
CC OC NCBI_TaxID=9913;
CC RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=98146173; PubMed=9486768;
RA Klump S., Selke D., Fischer D., Baumann A., Mueller F., Thanos S.;
RT "protein phosphatase type-2C isoforms present in vertebrate retinae;
RT purification, characterization, and localization in photoreceptors.";
RL J. Neurosci. Res. 51:328-338(1998).
CC -1- FUNCTION: Enzyme with a broad specificity.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: Binds 2 magnesium or manganese ions.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the PP2C family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ005457; CA06554.1; --
CC HSP; P35813; 1A6Q.
CC DR InterPro; IPR001932; PP2C-like.
CC DR InterPro; IPR000222; PP2C.
CC DR Pfam; PF00481; PP2C; 1.
CC DR SMART; SM00331; PP2C_SIG; 1.
CC DR SMART; SM00332; PP2C; 1.
CC DR PROSITE; PS01032; PP2C; 1.
CC DR PROSITE; PS01032; PP2C; 1.
CC KW Hydrolase; Magnesium; Manganese; Multigene family.
CC FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
CC FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
CC FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
CC FT METAL 239 239 MANGANESE 2 (BY SIMILARITY).
CC FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
CC SQ SEQUENCE 382 AA; 42529 MW; A716B3FA0E7E21C2 CRC64;
CC -----
CC Query Match 16.9%; Score 342; DB 1; Length 382;
CC Best Local Similarity 33.7%; Pred. No. 2.1e-17;
CC Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;
CC
CC QY 106 GLGYVAERGEREEMQDAHVILNDITECRPSSLIITVSVFAPDGHGIRASFAAQ 165
CC DB 21 GLAYGLSSQGVREVEDAHTAVIGL-----PSGLET-WSFPAVDGHAGSVAKYCCE 73
CC
CC QY 166 NLHQNLRKPP-KGD--VISVEKTVKRLDTEKHTDEBFLKQASSQKPAWKDGSTATCV 222
CC DB 74 HLLDHTNNQDPKSGAGAPSV-NVKNGITRTGFLDEHVRVMSKKHGDGRSGTAVGV 132
CC QY 223 LAVDNILYIANLGDSRAILCRYNESQKHAALSLSKEHNPTQYERWRIQAGNVDRGR 282
CC DB 133 LISPOHTYFTNCGDSRGLICR-----NRKVYFTQDHRKPSNPLEKRIQAGGSVMIOR 186
CC QY 283 VLGVLEVSISIGDQYKRC---GVT-----SVPDIRRCQLTENDRPFILLACDGLFK 330
CC DB 187 VNGSLAVSRALGDFDYK-CVHGKGPTEQLVSPPEVHDIERSE--EDDQFIILACDGIWD 243
CC QY 331 VFTPEAVNFILSCLE--DEKIQTRGKSAADARYEACNRLANKAVQSGSADNVTVWV 388
CC DB 244 VMGNEELCDFVRSRLVTD-----LEKVCNEVVDTCLYKGRDNMSVILI 289
CC
CC RESULT 8
CC FEM2_RAT
CC ID_FEM2_RAT STANDARD; PRT; 450 AA.
CC AC Q9WV7;
CC DT 28-FEB-2003 (Rel. 41, Created)
CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Ca(2+)/calmodulin-dependent protein kinase phosphatase (EC 3.1.3.16)
CC DE (CaM-kinase phosphatase) (CaMKPase) (Partner of PIX 2) (Protein
CC DE phosphatase 1P).

QY 327 GLFKVTPTEAVNFILSCLEDEKIQTRGKGAADARYEAACNRLANKAVQSGADNVTVM 386
DB 357 GFDFVPPHPIPLVGHLLRQK---GSGMHVAE-----ELVAVARDRGSHDNITVM 405
QY 387 VV 398
DB 406 VV 407

RESULT 9
P2CA_RABIT
ID P2CA_RABIT STANDARD; PRT; 382 AA.
AC P35814;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
DE (Protein phosphatase 1A).
DE PPM1A OR PPM1A.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92182001; PubMed=1311954;
RA Mann D.J., Campbell D.G., McGowan C.H., Cohen P.T.W.;
RT "Mammalian protein serine/threonine phosphatase 2C: cDNA cloning and
RT comparative analysis of amino acid sequences.";
RL Biochim. Biophys. Acta 1130:100-104(1992).
CC -!- FUNCTION: Enzyme with a broad specificity.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the PP2C family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; S87757; AAB21783.1; -.
DR PIR; S22422; S22422.
DR HSP; P35813; IAA60.
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Multigene family.
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 239 239 MANGANESE 2 (BY SIMILARITY).
FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
SQ SEQUENCE 382 AA; 42462 MW; 46SCF1854FDIC86 CRC64;

Query Match 16.8%; Score 340; DB 1; Length 382;
Best Local Similarity 33.7%; Pred. No. 2.9e-17;
Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;

QY 106 GLGKYVAERKGEREEMQDAHVILNDITECRPPSSLIITVSVFVDPDGGGRASKFAAQ 165
DB 21 GLAYGLSSMQGWRVEMEDAHTAVIGL-----PSGLET-WSFFAVYDGHAGSQVAKYCE 73
QY 166 NLHQNIRKPP-KGD--VISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGSTATCV 222

GN PPM1F OR POPX2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99279559; PubMed=10348902;
RA Kitani T., Ishida A., Okuno S., Takeuchi M., Kameshita I.,
RA Fujisawa H.;
RT "Molecular cloning of Ca2+/Calmodulin-dependent protein kinase
RT phosphatase.";
RL J. Biochem. 125:1022-1028(1999).
CC -!- FUNCTION: Dephosphorylates and concomitantly deactivates Cam-
CC kinase II activated upon autophosphorylation, and Cam-kinases IV
CC and I activated upon phosphorylation by Cam-kinase kinase.
CC Promotes apoptosis.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
CC -!- SUBUNIT: Associates with F1A1alpha (By similarity).
CC -!- SIMILARITY: Belongs to the PP2C family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB023634; BAA82477.1; -.
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Apoptosis; Multigene family.
FT DOMAIN 99 109 POLY-GLU.
FT METAL 356 356 MANGANESE 2 (BY SIMILARITY).
FT METAL 400 400 MANGANESE 2 (BY SIMILARITY).
SQ SEQUENCE 450 AA; 49165 MW; 67626542F32B2FD0 CRC64;

Query Match 16.9%; Score 341.5; DB 1; Length 450;
Best Local Similarity 29.4%; Pred. No. 2.8e-17;
Matches 124; Conservative 63; Mismatches 160; Indels 75; Gaps 16;

QY 3 LFGDLPEPSPRPAAGKAQKGPILLFDDLPASSTDSGSGGPLLFDLPASSGDSGL 62
DB 25 LLDQFPALSLSPLPWK--VPGTVLQGEVEAEITELAMGF-LGSRNAPPAVA--AAVT 79
QY 63 ATSIQMVKTEKGAKRTSEENKNGSE-----LVEKK-----VCKASSVI 104
DB 80 HEAISQLQTLSEFKRLPEQEVEEERVLTLDDAKGLSRFFNCLMEVCSQWQKR 139
QY 105 FGLKGYVAERK-----GEREMQDAHVILNDITECRPPSSLIITRV8-----YEA 149
DB 140 VELTAQAPQKWLVAIHAIRNTRKMDRHVSL-----PAPNHLFGLSDSVHRAYFA 191
QY 150 VFDGEGGRIRASKFAAQNLHONLIRFPKGDVISEKTVKRCLLDTFKHTDEEFLKQASSQ 209
DB 192 VFDGEGGVDAARYASVHVTHNASHQ-PE-----LLTDPAAALKAFRHTDQMFQAKRE 245
QY 210 KPAWKDGSTATCVLAVDNIYLIANTLGDRAILCRYNEESQKHAALSISKEINPTQYERM 269
DB 246 R--LQSGITGVCAITGAALHVAWLGDQSIVLV-----QQQVVKLMPEKPKPERQDEKS 297
QY 270 RIQKAGGNVR---DGRVJGVLEVSRIQGGQVKRGVTSVDIRRCQLTQPNDRILLACD 326
DB 298 RIEALGGFVSLMDCWRVNGTAVLSAIGD-VFQKPYVSGEADAASRELTGLEDYILLACD 356

QY 106 GLKGYVAERKGBREEMQDAHVILNDITEBCRPSSLIITVSYFNPVFDHGGRASKFAAQ 165
 DB 21 GLRYGLSSMQGWRVEMEDAHVIGL-----PSGLT-WSPFVYDGHAGSQVAKYCB 73
 QY 166 NLHQNLIRKFP-KGD--VISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGSTATCV 222
 DB 74 HLDHITNNQDFKSGAGAPSVB-NVKNIGRTGFLIDEHMRVMSKKHGADRSSTAVGV 132
 QY 223 LAVDNILYIANLGDGSRILCRVNEESQKHAALSLSKEHNPTQYVEMRIOKAGNVDRGR 282
 DB 133 LISPQHTYFINGDSRGLLCLR-----NRKVHFFTDQHKFSPNLEKRIQAGGSVMIO 186
 QY 283 VLGVLEVSRSIGDQYKRC-----GVT-----SVPDIRCOLTENDRIFILLACDGLFK 330
 DB 187 VNGSLAVSRALGDFDYK-CVHGKGPTEQLVSPPEVHDIERSE--EDDQFIILACDGIWD 243
 QY 331 VTPPEAVNFILSLB--DEKIQTRGSKAADARVEAACNRLANKAVQGSADNVTVMVV 388
 DB 244 VMGNEELCDFVRSRLVETDD-----LEKVCNEVVDTCLYKGRDNMNVILLI 289

RESULT 11
 ID P2CA MOUSE STANDARD; PRT; 382 AA.
 AC P49443;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
 DE (Protein phosphatase 1A).
 GN PPM1A OR PPM1A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RC MEDLINE=94333828; PubMed=8056349;
 RA Kato S., Kobayashi T., Terasawa T., Ohnishi M., Sasahara Y.,
 RA Kanamaru R., Tamura S.;
 RT "The cDNA sequence encoding mouse Mg2+ -dependent protein phosphatase
 RT alpha.";
 RL Gene 145:311-312(1994).
 RN SEQUENCE FROM N.A.
 RP STRAIN=FVB/N; TISSUE=Mammary gland;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Schuler G.D.,
 RA Altschul S.F., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Usdin T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Snerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Enzyme with a broad specificity.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- COFACTOR: Binds 2 magnesium or manganese ions.
 CC -!- SUBUNIT: Monomer.
 CC -!- SIMILARITY: Belongs to the PP2C family.

DB 74 HLDHITNNQDFKSGAGAPSVB-NVKNIGRTGFLIDEHMRVMSKKHGADRSSTAVGV 132
 QY 223 LAVDNILYIANLGDGSRILCRVNEESQKHAALSLSKEHNPTQYVEMRIOKAGNVDRGR 282
 DB 133 LISPQHTYFINGDSRGLLCLR-----NRKVHFFTDQHKFSPNLEKRIQAGGSVMIO 186
 QY 283 VLGVLEVSRSIGDQYKRC-----GVT-----SVPDIRCOLTENDRIFILLACDGLFK 330
 DB 187 VNGSLAVSRALGDFDYK-CVHGKGPTEQLVSPPEVHDIERSE--EDDQFIILACDGIWD 243
 QY 331 VTPPEAVNFILSLB--DEKIQTRGSKAADARVEAACNRLANKAVQGSADNVTVMVV 388
 DB 244 VMGNEELCDFVRSRLVETDD-----LEKVCNEVVDTCLYKGRDNMNVILLI 289

RESULT 10
 ID P2CA RAT STANDARD; PRT; 382 AA.
 AC P20650;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
 DE (Protein phosphatase 1A).
 GN PPM1A OR PPM1A OR PP2C1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Kidney;
 RC MEDLINE=89184515; PubMed=2538815;
 RA Tamura S., Lynch K.R., Lerner J., Fox J., Yasui A., Kikuchi K.,
 RA Suzuki Y., Tsuki S.;
 RT "Molecular cloning of rat type 2C (IA) protein phosphatase mRNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1796-1800(1989).
 CC -!- FUNCTION: Enzyme with a broad specificity.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- COFACTOR: Binds 2 magnesium or manganese ions.
 CC -!- SUBUNIT: Monomer.
 CC -!- SIMILARITY: Belongs to the PP2C family.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch)

EMBL: J04503; AAA1917.1;
 PIR: A32399; A32399.
 HSP: P35813; IAGQ.
 InterPro: IPR001932; PP2C-like.
 InterPro: IPR000222; PP2C.
 Pfam: PF00481; PP2C; 1.
 SMART: SM00331; PP2C SIG; 1.
 SMART: SM00332; PP2CC; 1.
 DR PROSITE: PS01032; PP2C; 1.
 KW Hydrolase; Magnesium; Manganese; Multigene family.
 FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
 FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
 FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 239 239 MANGANESE 2 (BY SIMILARITY).
 FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
 SQ SEQUENCE 382 AA; 42416 MW; C1C386B935374F89 CRC64;

Query Match
 Best Local Similarity 33.7%; Pred. No. 2.9e-17;
 Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;

CC CC -1- SIMILARITY: Belongs to the PP2C family.

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC CC the European Bioinformatics Institute. There are no restrictions on its

CC CC use by non-profit institutions as long as its content is in no way

CC CC modified and this statement is not removed. Usage by and for commercial

CC CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC CC or send an email to license@isb-sib.ch).

CC CC -----

CC DR EMBL; D28117; BAA05662.1; -

CC DR EMBL; BC008595; AAH08595.1; -

CC DR PIR; I53823; I53823.

CC DR HSP; P35813; IA6Q.

CC DR MGD; MGI:99878; Ppm1a.

CC DR InterPro: IPR001932; PP2C-like.

CC DR InterPro: IPR000222; PP2C.

CC DR Pfam; PF00481; PP2C; 1.

CC DR SMART; SM00331; PP2C_SIG; 1.

CC DR PROSITE; PS01032; PP2C; 1.

CC DR PROSITE; PS01032; PP2C; 1.

CC KW HydroLase; Magnesium; Manganese; Multigene family.

CC FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).

CC FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).

CC FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).

CC FT METAL 239 239 MANGANESE 2 (BY SIMILARITY).

CC FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).

CC SQ SEQUENCE 382 AA; 42432 MW; DC206610E1583870 CRC64;

CC Query Match 16.7%; Score 338; DB 1; Length 382;

CC Best Local Similarity 33.0%; Pred. No. 4e-17;

CC Matches 99; Conservative 47; Mismatches 106; Indels 48; Gaps 11;

CC QY 106 GLKGYVAERGEREMQDAHVINDITECRPSSILITRVSYFAVDFGCGITRASFQAQ 165

CC DB 21 GLRYGLSMQGWREMDAHTAVIGL-----PSGLET-WSFFAVYDGHAGSQVAKYCC 73

CC QY 166 NLHQNLIRKFP---KGDVSVKTVKRCLLDTFCHTDEEFLKQASSQKPAWKDGSTATCV 222

CC DB 74 HLDHITNNQDFRSGAGAPSV-NVKGIRGTGFLDEHVRVNSEKKGHADRSGSTAVGV 132

CC QY 223 LAVDNILYIANLGDRAILCRYNESQKHAALSKEHNPTQYEERMRIQKAGNVRDGR 282

CC DB 133 LISQHYFFYFNGDSRGLLGR-----NRKVHFTQDHPKSNPLEKRIQAGSVMIQR 186

CC QY 283 VLGVLVSRIIGDQYKRC-----SVPTDIRCOLTPNDFILLACDGLFK 330

CC DB 187 VNGSLAVSRALGDPDYK-CVHGKGPTEQLVSPPEVHDIERSE--EDDQFIILACDGIWD 243

CC QY 331 VFTPEEAVNFILSCLE--DEKIQTRCKSADADRYEACNRLANKAVQSGADNVTVMVV 388

CC DB 244 VMGNEELCDFVRSLEVTDD-----LEKVCNEVVDTCLYKSGRDNMSVILI 289

CC RESULT 12

CC P2CA HUMAN STANDARD; PRT; 382 AA.

CC AC P35813; 075551;

CC DT 01-JUN-1994 (Rel. 29, Created)

CC DT 01-JUN-1994 (Rel. 29, Last sequence update)

CC DT 10-OCT-2003 (Rel. 42, Last annotation update)

CC DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)

CC DE (Protein phosphatase 1A).

CC GN PPM1A OR PPM1A.

CC OS Homo sapiens (Human).

CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

CC OX NCBI_TaxID=9606;

CC [1]

CC RP SEQUENCE FROM N.A. (ISOFORM ALPHA-1).

CC RX MEDLINE=92182001; PubMed=1311954;

CC RA Mann D.J., Campbell D.G., McGowan C.H., Cohen P.T.W.;

CC RT "Mammalian protein serine/threonine phosphatase 2C: cDNA cloning and

RT comparative analysis of amino acid sequences.";

RL Biochim. Biophys. Acta 1130:100-104(1992).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM ALPHA-2).

RX MEDLINE=98372738; PubMed=9707433;

RA Takekawa M., Maeda T., Saito H.;

RT "Protein phosphatase 2Calpha inhibits the human stress-responsive p38

RT and JNK MAPK pathways.";

RL EMBO J. 17:4744-4752(1998).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM ALPHA-1).

RN TISSUE=Colon;

RC MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickens M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [4]

RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).

RX MEDLINE=97157470; PubMed=9003755;

RA Das A.K., Helps N.R., Cohen P.T.W., Barford D.;

RT "Crystal structure of the protein serine/threonine phosphatase 2C at

RT 2.0-A resolution.";

RL EMBO J. 15:6738-6809(1996).

CC -1- FUNCTION: Enzyme with a broad specificity.

CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +

CC phosphate.

CC -1- COFACTOR: Binds 2 magnesium or manganese ions.

CC -1- SUBUNIT: Monomer.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=Alpha-1;

CC IsoId=P35813-1; Sequence=Displayed;

CC Name=Alpha-2;

CC IsoId=P35813-2; Sequence=VSP_005085, VSP_005086;

CC -1- SIMILARITY: Belongs to the PP2C family.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; S87759; AAB21784.1; -

CC EMBL; AR076670; AAC28354.1; -

CC EMBL; BC026691; AAH26691.1; -

CC PIR; S22423; S22423.

CC Genew; HGNC:9275; PPM1A.

CC MIM; 606108; -

CC PDB; 1AQJ; 27-MAY-98.

CC GO; GO:0015071; F:protein phosphatase type 2C activity; TAS.

CC InterPro; IPR001932; PP2C-like.

CC InterPro; IPR000222; PP2C.

CC Pfam; PF00481; PP2C; 1.

CC SMART; SM00331; PP2C_SIG; 1.

DR SMART; SMO0332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Multigene family;
KW Alternative splicing; 3D-structure.
FT METAL 37 38
FT METAL 38 38
FT METAL 60 60
FT METAL 239 239
FT METAL 282 282
FT METAL 318 324
FT VARSPLIC 325 382
FT VARSPLIC 325 382
FT STRAND 9 19
FT TURN 20 21
FT STRAND 22 31
FT TURN 22 31
FT STRAND 32 32
FT TURN 32 32
FT STRAND 38 46
FT TURN 38 46
FT STRAND 47 49
FT TURN 47 49
FT STRAND 50 62
FT TURN 50 62
FT STRAND 66 80
FT TURN 66 80
FT STRAND 81 81
FT TURN 81 81
FT STRAND 83 86
FT TURN 83 86
FT STRAND 94 118
FT TURN 94 118
FT STRAND 119 120
FT TURN 119 120
FT STRAND 126 127
FT TURN 126 127
FT STRAND 129 134
FT TURN 129 134
FT STRAND 138 144
FT TURN 138 144
FT STRAND 148 153
FT TURN 148 153
FT STRAND 154 155
FT TURN 154 155
FT STRAND 156 160
FT TURN 156 160
FT STRAND 166 167
FT TURN 166 167
FT STRAND 169 177
FT TURN 169 177
FT STRAND 178 179
FT TURN 178 179
FT STRAND 182 183
FT TURN 182 183
FT STRAND 184 185
FT TURN 184 185
FT STRAND 186 187
FT TURN 186 187
FT STRAND 188 190
FT TURN 188 190
FT STRAND 191 191
FT TURN 191 191
FT STRAND 195 195
FT TURN 195 195
FT STRAND 197 198
FT TURN 197 198
FT STRAND 200 202
FT TURN 200 202
FT STRAND 206 207
FT TURN 206 207
FT STRAND 210 212
FT TURN 210 212
FT STRAND 216 216
FT TURN 216 216
FT STRAND 220 225
FT TURN 220 225
FT STRAND 228 230
FT TURN 228 230
FT STRAND 231 237
FT TURN 231 237
FT STRAND 239 242
FT TURN 239 242
FT STRAND 243 244
FT TURN 243 244
FT STRAND 247 258
FT TURN 247 258
FT STRAND 259 260
FT TURN 259 260
FT STRAND 264 277
FT TURN 264 277
FT STRAND 278 279
FT TURN 278 279
FT STRAND 284 290
FT TURN 284 290
FT STRAND 292 293
FT TURN 292 293
FT STRAND 299 319
FT TURN 299 319
FT STRAND 330 339
FT TURN 330 339
FT STRAND 340 341
FT TURN 340 341
FT STRAND 347 349
FT TURN 347 349
FT STRAND 350 354
FT TURN 350 354
FT STRAND 355 365
FT TURN 355 365
FT SEQUENCE 382 AA; 42447 MW; D48EF508B4A76687 CRC64;
Query Match 16.7%; Score 336; DB 1; Length 382;
Best Local Similarity 33.3%; Pred. No. 5.6e-17;
Matches 100; Conservative 47; Mismatches 105; Indels 48; Gaps 12;
QY 106 GLKGYVAERKGRBEMQDAHVILNDITBECRPPSLITRVYFAVFDGHGIRASKFAAQ 165
DB 21 GLRYGLSSMQGRVEMEDAHTAVIGL-----PSGL-ESWSFFAVYDGHAGSQVAKYCC 73
QY 166 NLHQNLIRKFP-KGD--VISVEKTVKRCILDTFFKHTDEFLKQASSQKPAKDGSTATCV 222

Db 74 HLLDHTNNQDFKGSAGAPSVN-VNKGIRITGFLDEHMRVMSEKKGADRSSTAVGV 132
QY 223 LAVDNILYIANLGDRAILCRVNEESQHAALSLSKEHNPTQYERMRIOKAGGNVDRGR 282
Db 133 LISPOHTYFINGDSRGLLCR-----NRKVHFFTDQHKPSNPLEKRIQNAAGSVMIQR 186
QY 283 VLGVLEVSRSIGDQYKCC---GVT-----VPPDIRRCQLTPNDRFILLACDGLPK 330
Db 187 VNGSLAVSALGDFDYK-CVHGKGTPEQLVSPPEVHDIERSE--EDQFILLACDGIWD 243
QY 331 VFTPEAVNFIILSCLE--DEKIQITREGKSAADARYEAACNRLANKAVORGSDNVTVMV 388
Db 244 VMGNEELCDFVSRLEVTDD-----LEKVCNEVVDTCLYKGRSDNNMSVILI 289

RESULT 13
P2C2 ARATH STANDARD; PRT; 423 AA.
AC 004719;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C ABI2 (EC 3.1.3.16) (PP2C) (Abscisic acid-insensitive 2).
GN ABI2 OR ATSG57050 OR MHM17.19.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;
OC eusoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia, and cv. Landsberg erecta;
RX MEDLINE=97308526; PubMed=9165752;
RA Leung J., Merlot S., Giraudat J.;
RT "The Arabidopsis ABCISIC ACID-INSENSITIVE2 (ABI2) and ABI1 genes encode homologous protein phosphatases 2C involved in abscisic acid signal transduction.";
RL Plant Cell 9:759-771(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty P1 and TAC clones.";
RL DNA Res. 7:31-63(2000).
CC -I- FUNCTION: Involved in abscisic acid (ABA) signaling pathway.
CC -I- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.
CC -I- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
CC -I- SIMILARITY: Belongs to the PP2C family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y08966; CAA70163.1; -;
CC EMBL; Y08965; CAA70162.1; -;
CC EMBL; Y11840; CAA72538.1; -;
CC EMBL; AB024035; BAA97035.1; -;
DR

DR HSP; P35913; IA6Q.
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydroxylase; Magnesium; Manganese; Multigene family; Calcium-binding.
FT CA BIND 70 EF-HAND (POTENTIAL).
SQ SEQUENCE 423 AA; 46306 MW; 67CAAC76DA531A71 CRC64;

Query Match 16.5%; Score 333; DB 1; Length 423;
Best local similarity 29.3%; Pred. No. 1.1e-16;
Matches 118; Conservative 63; Mismatches 130; Indels 92; Gaps 19;

Qy 51 LPAS-SGDSG-----SLATSIQWVTEGKCAKKTSEEEKNGSEEL---- 92
Db 34 LPSSCGSGAMKDSFEINTRQSLTSSSAMAGVD-----ISAGDEINGSDEFPPS 87
Qy 93 --VEKKVCK--ASSVIFGLKGY---VAERKEREMQD-----AHVILND 130
Db 88 MNQSEKVLGRTSRSLFKECVLYGVTSICRRPEMEDSVSTIPRFQVSSSSLDGR 147
Qy 131 ITBECRPPSLITRVSVFVFDGHHGIRASKFAAQLNH-----QNLIRKFPK---GDVISV 183
Db 148 VTNGFNPHLS-----AHFFGVYDGGGSOVANYCRMHGLALTEIVKEKEPFCDGD--TW 201
Qy 184 EKVRCCLDTFHTDEEFLKQASSQKPAWKDGTATCVLAVNLIYIANLGDRAILCR 243
Db 202 QEKWKALFNFMRVDSIEITHAPETV---GSTSVAVVFPTHIFVANGDSRAVLCR 258
Qy 244 YNEESQHAALSLSKENPTQYERMRIOKAGNV---RGRVLGVLEVSRSIGDQYKR 300
Db 259 -----GKTPLALSVDPKDDAARIEAAGKVRWNGARVFGVLAWSRSIGD-RYLK 311
Qy 301 CGVTSVPDIRRCQLTNDRIILLACDGLFKVFTPEEAVNF-----IL-----SCL 345
Db 312 PSVIPDPEVTSVRVKEDDCLLASDGLWDMVNEEVCDAKRLILHWHKNMAGEALL 371
Qy 346 EDEKIQRGKSAADARYEAACNRLANKAVQGSADNVTVVWV 388
Db 372 PAEK--RGEK---DPAAMSAEVLKQALQKSKONISVVVV 409

RESULT 14
P2CB MOUSE
ID _P2CB MOUSE STANDARD; PRT; 390 AA.
AC P36993;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta) (IA)
DE (Protein phosphatase 1B).
GN PM1B OR PPM1B OR PP2C2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=9409616; PubMed=8274020;
RA Terasawa T., Kobayashi T., Murakami T., Ohnishi M., Kato S.,
RA Tanaka O., Kondo H., Yamamoto H., Takeuchi T., Tamura S.,
RT "Molecular cloning of a novel isotype of Mg(2+)-dependent protein
phosphatase beta (type 2C beta) enriched in brain and heart."
RL Arch. Biochem. Biophys. 307:342-349(1993).
RN [2]
RN SEQUENCE FROM N.A. (BETA-3; BETA-4 AND BETA-5).
RP TISSUE=Testis;
RC MEDLINE=95251388; PubMed=7733667;
RA Kato S., Terasawa T., Kobayashi T., Ohnishi M., Sasahara Y.,
RA Kusuda K., Yanagawa Y., Hiraga A., Matsui Y., Tamura S.,
RT "Molecular cloning and expression of mouse Mg(2+)-dependent protein

phosphatase beta-4 (type 2C beta-4).";
RL Arch. Biochem. Biophys. 318:387-393(1995).
RN [3]
RP SEQUENCE FROM N.A. (BETA-3 AND BETA-4).
RC TISSUE=Testis;
RX MEDLINE=94313028; PubMed=8038726;
RA Hou E.W., Kawai Y., Miyasaka H., Li S.S.;
RT "Molecular cloning and expression of cDNAs encoding two isoforms of
protein phosphatase 2C beta from mouse testis."
RL Biochem. Mol. Biol. Int. 32:773-780(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RX MEDLINE=99398339; PubMed=10469137;
RA Ohnishi M., Chida N., Kobayashi T., Wang H., Ikeda S., Hanada M.,
RA Yanagawa Y., Katsura K., Hiraga A., Tamura S.;
RT "Alternative promoters direct tissue-specific expression of the mouse
protein phosphatase 2C beta gene."
RL Eur. J. Biochem. 263:736-745(1999).
CC -!- FUNCTION: Enzyme with a broad specificity.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Comment=Isoforms only differ in their C-terminus;
CC Name=Beta-1;
CC IsoId=P36993-1; Sequence=Displayed;
CC Name=Beta-2;
CC IsoId=P36993-2; Sequence=VSP_005089;
CC Name=Beta-3;
CC IsoId=P36993-3; Sequence=VSP_005090;
CC Name=Beta-4;
CC IsoId=P36993-4; Sequence=VSP_005091;
CC Name=Beta-5;
CC IsoId=P36993-5; Sequence=VSP_005092;
CC -!- TISSUE SPECIFICITY: Beta-1 is expressed ubiquitously; beta-2 is
expressed exclusively in brain and heart; beta-4 is expressed
exclusively in brain and intestine; beta-3 and beta-5 are
expressed exclusively in testis and intestine.
CC -!- SIMILARITY: Belongs to the PP2C family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL; D17411; BAA04233.1; -
DR EMBL; D17412; BAA04234.1; -
DR EMBL; D45859; BAA08293.1; -
DR EMBL; D45860; BAA08294.1; -
DR EMBL; D45861; BAA08295.1; -
DR EMBL; U09218; AAB60442.1; -
DR EMBL; AB007798; BAA84471.1; -
DR EMBL; AB007794; BAA84471.1; JOINED.
DR EMBL; AB007795; BAA84471.1; JOINED.
DR EMBL; AB007796; BAA84471.1; JOINED.
DR EMBL; AB007797; BAA84471.1; JOINED.
DR PIR; I49016; I49016.
DR PIR; S65672; S65672.
DR HSSP; P35913; IA6Q.
DR MGD; MGI:101841; Ppm1b.
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Multigene family;

[illegible]

Qy 303 -VTSVPDIRCQTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKGAADA 361
Db 219 LVSPEPEVYELLRAEEDFVVLACDGIWDVMSNEELCEFNRL-----VSD 266
Qy 362 RYEAACNRLANKAVQSGADNVVMV 388
Db 267 DLENVCNWWDTCLHKGSRDNNMIVLV 293

Search completed: April 12, 2004, 09:06:41
Job time : 18 secs

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:03:32 ; Search time 45 Seconds
(without alignments)
2748.514 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 2018
Sequence: 1 MDLFGDLPEPRSPRAAGK.....KAVQGSADNVTVMVVRIGH 392

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2018	100.0	392	4	Q9H0C8 homo sapien
2	1935	95.9	392	11	Q8R0F6
3	1931	95.7	392	11	Q9Z1Z6
4	1078	53.4	212	11	Q9CS46
5	856	42.4	167	11	Q9Z0T2
6	728	36.1	385	5	Q86F00
7	481	23.8	341	10	Q9LMT1
8	480	23.8	351	10	Q944X0
9	474	23.5	242	5	O62212
10	408.5	20.2	319	10	Q8S8Z0
11	398.5	19.7	311	10	Q8RXV3
12	391	19.4	282	10	Q7XR05
13	381.5	18.9	243	10	Q8S3P1
14	370.5	18.4	354	10	Q8LAY8
15	368.5	18.3	420	10	Q8VZD9
16	368	18.2	319	5	Q7YUT1

RESULT 1

Q9H0C8

ID Q9H0C8 PRELIMINARY; PRT; 392 AA.

AC Q9H0C8; TREMBLrel. 16, Created

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Hypothetical protein (Integrin-linked kinase-associated

DE serine/threonine phosphatase 2C).

GN DKP2P34J2031.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]_

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RA Blum H., Bauersachs S., Mewes H.W., Weil B., Wiemann S.;

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Leung-Hageteijn C., Mahendra A., Naruszewicz I., Hannigan G.E.;

RT "Modulation of integrin signal transduction by ILKAP, a protein

phosphatase 2C associating with the integrin-linked kinase, ILK1.";

RL EMBO J. 0:0-0(2001).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Uterus;

RA Strausberg R.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.

DR EMBL; AL136850; CAB66784.1; -

DR EMBL; AY024365; AAK07735.1; -

DR HSSP; P35813; 1A6Q.

DR Genew; HGNC:15566; ILKAP.

DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.

DR GO; GO:0015781; F:hydrolase activity; IEA.

DR GO; GO:0016301; F:kinase activity; IEA.

ALIGNMENTS

17	368	18.2	389	10	O81773
18	368	18.2	975	5	O15743
19	366.5	18.2	420	10	Q94AT1
20	366.5	18.2	757	4	Q9UPT0
21	365	18.1	359	10	O82469
22	365	18.1	766	4	Q8WY54
23	364.5	18.1	348	10	Q9LEW5
24	364.5	18.1	371	10	Q8VZN9
25	362	17.9	464	10	Q9FXE4
26	361	17.9	380	10	Q8RX37
27	361	17.9	750	11	Q80Z30
28	359.5	17.8	388	10	Q8H610
29	358.5	17.8	361	10	Q9SD02
30	358.5	17.8	665	11	Q801L0
31	356	17.6	643	11	Q8CB81
32	353.5	17.5	355	10	O81716
33	353.5	17.5	362	10	Q9ZPL9
34	353.5	17.5	438	3	Q7Z8P2
35	352	17.4	307	10	Q9FGM3
36	352	17.4	392	10	Q9SLA1
37	351	17.4	404	10	O22200
38	351	17.4	658	10	Q940A2
39	350	17.3	305	10	Q942N4
40	350	17.3	357	10	Q9S253
41	342	16.9	439	3	Q872D8
42	340	16.8	1148	5	Q86A16
43	339	16.8	396	10	Q9LP12
44	338.5	16.8	383	10	Q9MLP8
45	338.5	16.8	390	10	Q9XEE8

O81773	arabidopsis
O15743	dictyosteli
Q94AT1	arabidopsis
Q9UPT0	homo sapien
O82469	mesembryant
Q8WY54	homo sapien
Q9LEW5	arabidopsis
Q8VZN9	arabidopsis
Q9FXE4	arabidopsis
Q8RX37	arabidopsis
Q80Z30	rattus norv
Q8H610	oryza sativ
Q9SD02	arabidopsis
Q801L0	mus musculu
Q8CB81	mus musculu
O81716	arabidopsis
Q9ZPL9	lotus japon
Q7Z8P2	trichodema
Q9FGM3	arabidopsis
Q9SLA1	arabidopsis
O22200	arabidopsis
Q940A2	arabidopsis
Q942N4	oryza sativ
Q9S253	arabidopsis
Q872D8	neurospora
Q86A16	dictyosteli
Q9LP12	arabidopsis
Q9MLP8	arabidopsis
Q9XEE8	arabidopsis

DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
DR KW Hypothetical protein; Hydrolase; Kinase; Magnesium.
SQ SEQUENCE 392 AA; 42906 MW; AF6ACC98508CBEA3 CRC64;

Query Match 100.0%; Score 2018; DB 4; Length 392;
Best Local Similarity 100.0%; Pred. No. 5.8e-154;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRAAGKAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
DB 1 MDLFGDLPEPERSPPRAAGKAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
QY 61 SLATSIQWVKTEGKAKRTSEEEKNGSEBELVEKKVKASSVIFGLKGYVAERKGEREE 120
DB 61 SLATSIQWVKTEGKAKRTSEEEKNGSEBELVEKKVKASSVIFGLKGYVAERKGEREE 120
QY 121 MQDAHVLNDITEECRPPSSLIITRYSYFAVFDGHHGIRASKFAAQNHLQNLIRKPKGDV 180
DB 121 MQDAHVLNDITEECRPPSSLIITRYSYFAVFDGHHGIRASKFAAQNHLQNLIRKPKGDV 180
QY 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDRAI 240
DB 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDRAI 240
QY 241 LCRYNEESQKHAALSLSKEHNPTQYEERMRICKAGNVDRDGRVLGVLEVSRSIGDGYKR 300
DB 241 LCRYNEESQKHAALSLSKEHNPTQYEERMRICKAGNVDRDGRVLGVLEVSRSIGDGYKR 300
QY 301 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
DB 301 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
QY 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392
DB 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392

RESULT 2
Q8R0F6 PRELIMINARY; PRT; 392 AA.
AC Q8R0F6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to protein phosphatase 2C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue-Liver;
RA Strausberg R.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
DR EMBL; BC026953; AAH26953.1; -!
DR GO; GO:0000287; F:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.

DR SMART; SM00331; PP2C SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
DR KW Hydrolase; Magnesium.
SQ SEQUENCE 392 AA; 42774 MW; 8DE1F77DAC9B7176 CRC64;

Query Match 95.9%; Score 1935; DB 11; Length 392;
Best Local Similarity 95.2%; Pred. No. 2.7e-147;
Matches 373; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRAAGKAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
DB 1 MDLFGDLPEPERSPPRAAGKAQKGLLFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
QY 61 SLATSIQWVKTEGKAKRTSEEEKNGSEBELVEKKVKASSVIFGLKGYVAERKGEREE 120
DB 61 SLATSIQWVKTEGKAKRTSEEEKNGSEBELVEKKVKASSVIFGLKGYVAERKGEREE 120
QY 121 MQDAHVLNDITEECRPPSSLIITRYSYFAVFDGHHGIRASKFAAQNHLQNLIRKPKGDV 180
DB 121 MQDAHVLNDITEECRPPSSLIITRYSYFAVFDGHHGIRASKFAAQNHLQNLIRKPKGDV 180
QY 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDRAI 240
DB 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDRAI 240
QY 241 LCRYNEESQKHAALSLSKEHNPTQYEERMRICKAGNVDRDGRVLGVLEVSRSIGDGYKR 300
DB 241 LCRYNEESQKHAALSLSKEHNPTQYEERMRICKAGNVDRDGRVLGVLEVSRSIGDGYKR 300
QY 301 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
DB 301 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
QY 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392
DB 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392

RESULT 3
Q9Z1Z6 PRELIMINARY; PRT; 392 AA.
AC Q9Z1Z6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein phosphatase 2C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99074314; PubMed=9857069;
RA Tong Y.; Quirion R.; Shen S.H.;
RT "Cloning and characterization of a novel mammalian PP2C isozyme.";
RL J. Biol. Chem. 273:35282-35290(1998).
CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
DR EMBL; AF095927; AAC97497.1; -!
DR HSSP; P35813; 1A6Q.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
DR KW Hydrolase; Magnesium.
SQ SEQUENCE 392 AA; 42744 MW; 1468FDE0BA60D915 CRC64;

Query Match 95.7%; Score 1931; DB 11; Length 392;
Best Local Similarity 95.2%; Pred. No. 5.8e-147;
Matches 373; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERPRPAAGKEAQKGLLFDLLPASSTDSGGPPLFDLLPPASSGDSG 60
DB 1 MDLFGDLPEPERPRPSAGKEAQEGPVLFDLPTSTDSGGPPLFDLPPAGSNGS 60

QY 61 SLATSIQMWKTKGKAKRTISEENKNGSEELVEKKVCKASSVIFGLKYVAERGEREE 120
DB 61 SLATSGQVVKNEKGAKRKAPEEENKNGSEELVEKKVCKASSVIFGLKYVAERGEREE 120

QY 121 MQDAHVLNDITRECPSPSLITRVSYFAVFDGHHGIRASKFAAQNHLNLRKPKGDV 180
DB 121 MQDAHVLNDITRECPSPSLITRVSYFAVFDGHHGIRASKFAAQNHLNLRKPKGDV 180

QY 181 ISVEKTVKRCCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDRAI 240
DB 181 ISVEKTVKRCCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDRAI 240

QY 241 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVDRGVLGVLEVSRSIGDQYKR 300
DB 241 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVDRGVLGVLEVSRSIGDQYKR 300

QY 301 CGVTSVPDIRCOLTPNDRIFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
DB 301 CGVTSVPDIRCOLTPNDRIFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360

QY 361 ARYEACNRLANKAVORGSDNVTVMVRIGH 392
DB 361 ARYEACNRLANKAVORGSDNVTVMVRIGH 392

RESULT 4
Q9CS46 PRELIMINARY; PRT; 212 AA.

AC Q9CS46;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 0710007A14RIK protein (Fragment).
GN 0710007A14RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinesawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staehli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sakai H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyrshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK019158; BAB31574.1; -.
DR HSSP; P35813; 1A6Q
MGD; MGI:1914694; 0710007A14RIK.

GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR001932; PF2C-like.
Pfam; PF00481; PF2C; 1.
DR SMART; SM00332; PF2C; 1.
FT NON TER 1
SQ SEQUENCE 212 AA; 23615 MW; 133286D628B540D7 CRC64;

Query Match 53.4%; Score 1078; DB 11; Length 212;
Best Local Similarity 98.1%; Pred. No. 9.8e-79;
Matches 208; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 181 ISVEKTVKRCCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDRAI 240
DB 1 ISVEKTVKRCCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDRAI 240

QY 241 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVDRGVLGVLEVSRSIGDQYKR 300
DB 61 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVDRGVLGVLEVSRSIGDQYKR 120

QY 301 CGVTSVPDIRCOLTPNDRIFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
DB 121 CGVTSVPDIRCOLTPNDRIFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360

QY 361 ARYEACNRLANKAVORGSDNVTVMVRIGH 392
DB 181 ARYEACNRLANKAVORGSDNVTVMVRIGH 212

RESULT 5
Q920T2 PRELIMINARY; PRT; 167 AA.

AC Q920T2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN 0710007A14RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Stothard P.M., Pilgrim D.;
RT "Isolation of P2C sequences using degenerate-oligo PCR."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF117831; AAD17234.1; -.
DR HSSP; P35813; 1A6Q.
MGD; MGI:1914694; 0710007A14RIK.
GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR001932; PF2C-like.
Pfam; PF00481; PF2C; 1.
DR SMART; SM00332; PF2C; 1.
KW Hypothetical protein.
FT NON TER 1
FT NON TER 167
SQ SEQUENCE 167 AA; 18795 MW; 3A4FC2EFB09DD95B CRC64;

Query Match 42.4%; Score 856; DB 11; Length 167;
Best Local Similarity 98.8%; Pred. No. 5e-61;
Matches 165; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 157 IRASKFAAQNHLNLRKPKGDVISEKTVKRCCLLDTFKHTDEEFLKQASSQKPAWKD 216
DB 1 IRASKFAAQNHLNLRKPKGDVISEKTVKRCCLLDTFKHTDEEFLKQASSQKPAWKD 60

QY 217 STATCVLAVDNILYIANLGDRAILCRYNESQKHAALSLSKEHNPTQYERMRIOKAG 276
DB 61 STATCVLAVDNILYIANLGDRAILCRYNESQKHAALSLSKEHNPTQYERMRIOKAG 120

QY 277 NVDRGVLGVLEVSRSIGDQYKRCGVTSVPDIRCOLTPNDRIFILL 323

```
Db 121 NVDRGVLVGVLEVSRSIGGGYKRCGVTSVPDIRRCQLTPNDRFILL 167
RESULT 6
Q86F00
ID Q86F00 PRELIMINARY; PRT; 385 AA.
AC Q86F00;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Clone ZD1250 mRNA sequence.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
SEQUENCE FROM N.A.
RA Liu F., Hu W., Yan Q., Xu X., Zhu Z., Zhang X., Wang J., Sun J.,
RA Xu X., Wang Z., Zeng L., Xiong Y., Wu X., Qu J., Xu Z., Huang J.,
RA Ma Y., Wang S., Wang X., Xue C., Feng Z., Chen Z., Han Z.;
RT "The full-length cDNA of S. japonicum Genes.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY223064; AAP06087.1; -.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 385 AA; 43372 MW; 74D60E17D11073EE CRC64;

Query Match 36.1%; Score 728; DB 5; Length 385;
Best Local Similarity 40.3%; Pred. No. 3.3e-50;
Matches 153; Conservative 62; Mismatches 91; Indels 74; Gaps 6;

QY 47 LPDDLPPASSGSGSLATSIQMKVTEGKAKRTSEEEKNGSEELVEKK----- 96
Db 3 LFDLLPEPS-----VESDEIQKSETLIEDSSWNEPESVSK 37
QY 97 ---VCKASSVIFGLKGVVAERKGERBERMDAHVLNDITEC-RPSSLLITRVSFAVF 151
Db 38 ITPFTCS-----VARKGRPEMQDSHIVVDNLADSMRPGVSEILRVCFYFVF 86
QY 152 DGHGIRASKFAAQNHLKRPKPGDVISVEKTKRCLLDTFKHTDEBFLKQASSQKP 211
Db 87 DGHGAKAANFACKELHDIARFPRGGIQQVEKDKKVLDSYKTKTDEBFLKQASSQKP 146
QY 212 AWKDGSTATCVLAVNLIYANLGDRAILCRYNE-----ESQKHAALS 255
Db 147 HWRDGSTAATILLVNDTLYIGNLGDVKVLLARVLESLSSESNPNVNGNILLSKLSAIC 206
QY 256 LSKHNPTQYERMPRIQAGNVRDGRVGLVLEVSRSIGDQYKRCGVTSVPDIRRCQLT 315
Db 207 LTKDNPNVDYERQRIQATGASVQNGRYSVLEVSRSFGDYQFKQGVTCIPDVRKQCLT 266
QY 316 NDRFILLACDGLPKVTPPEAVNFILSCL-----EDEKIQTRREGKSAADARYEAACN 368
Db 267 NDQFLLACDGLKWSFPDPAVHLTHRLMQEIKNHENQKSKNQDQIFQCRHLDVSVA 326
QY 369 RLANKAVQRGADNVTVMVV 388
Db 327 HLIVNEAVLRMSGDNVTICILL 346

RESULT 7
Q9LMT1
ID Q9LMT1 PRELIMINARY; PRT; 341 AA.
AC Q9LMT1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

Db 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE T10F20.4 protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RA Sakano H., Liu S.X., Etgu P., Lee J.M., Lenz C., Pham P., Toriumi M.,
RA Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A., Vaysberg M.,
RA Altati H., Brooks S., Buehler B., Chao Q., Conn L., Conway A.B.,
RA Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
RA Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
RA Rederspiel N.A., Theologis A.;
RT "The sequence of BAC T10F20 from Arabidopsis thaliana chromosome 1.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC034107; AAF97840.1; -.
DR PIR; G86315; G86315.
DR HSP; P35813; 1A60.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C SIG; 1.
SQ SEQUENCE 341 AA; 37367 MW; 6873C0CE82310195 CRC64;

Query Match 23.8%; Score 481; DB 10; Length 341;
Best Local Similarity 35.8%; Pred. No. 2e-30;
Matches 119; Conservative 66; Mismatches 107; Indels 40; Gaps 11;

QY 78 KBKTSEEEKNGSEELV-----EKKYCKASSVI-----FGLKGVVAERKGERBERMDAHVI 127
Db 24 KAKKSEVSGGGEAAVAGNREAEEDKPSFSEKKEFLVEADVAEDKGRGARTMEDVWVV 83
QY 128 LNDITEECRPSLLITRVSFAVFEDHGIGIRASKFAAQNHLKRPKPGDVISVEKTKV 187
Db 84 LPDASLDF--PQTL--RCAHFAIYDGHGRLAAEFKXHLHUNLVISAGLPRELLDV-KVA 138
QY 188 KRCLLDTFKHTDEEFLKQASSQKPAGKDGSTATCVLAVNLIYANLGDRAILCR---- 243
Db 139 KKAILEGFKTKTDELLQKSVS--GGQDQATAVCWILDQKVFVANIGDAKAVLARSSVT 196
QY 244 -----YNESQKHAALSLSKEHNPTQYERMPRIQAGNVRDGRVGLVLEVSRSIGDQ 297
Db 197 NELGNHTEAGNPLKAIVLTRHKAIYQPSRSIQKSGGVISSNGRIQGRLEYSRAFGRH 256
QY 298 YKRCGVTSVPDIRRCQLTENDRIFILLACDGLPKVTPPEAVNFILSCLDEKIQTRREGK 357
Db 257 FKFGVSAFPIHAFELTERENFMILGCDGLWEVFGPSDAVGFQKLL-----KEG-- 307
QY 358 AADARYEAACNRLANKAV-ORGSADNVTVMVV 388
Db 308 ----LHVSTVSRRLVKEAVKERRCKNCTAIVI 336

RESULT 8
Q944K0
ID Q944K0 PRELIMINARY; PRT; 351 AA.
AC Q944K0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Atg18030/T10F20.3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
```



```

RESULT 9
ID O62212
AC O62212; PRELIMINARY; PRT; 242 AA.
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE F33A8.6 protein.
GN F33A8.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RP Matthews L.;
RA Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

```

Query Match	23.5%;	Score	474;	DB	5;	Length	242;	
Best Local Similarity	40.2%;	Pred.	No. 4.6e-30;					
Matches	98;	Conservative	54;	Mismatches	80;	Indels	12; Gaps	5;
Qy	82	SBEKNGSRLV---	EKKVKASSVLGLGVYABRKGBREMQDAHVILN--	DITEEC	135			
Db	3	SDSRKRSSDDLIDNSDESKPKESRNDLYCTLAAYGCRKGBRADMQDTHIMLPKFDLGTGTE-	61					
Qy	136	RPPSSLITRVSYFAVDGHGGIRASKFAAQNHLQRNLIRKEPK-GDVTSVBKTAVARCLLDT	194					
Db	62	---KSFLSRASFPATPDGHAGPRAAHCSQMGKTVKEKLAKTSPFTLLFKSLKQTETES	118					
Qy	195	KRHTDEEFLKQASSQXPAWKDGSTATCVLAVDNILYIANJGDSRAILCRYNESQKHAAAL	254					
Db	119	YKAVDDGFLALAKNQKPIMKDGGTTATTMIILNNVIIVANIGDSRAVVARKEDG-SFAPV	177					
Qy	255	SIISKENPTQYBERMIOKAGGNVRGRVLGVLEVSRSIGDGYKRCGVTVSVDPDIRCQL	314					
Db	178	CLTVDDHPMSHDERMAIKAGAVVKDGRINGVIEVRSISIGDLFPFKSLGIISTPDLKKLTLL	237					
Qy	315	TPND	318					
Db	238	TKND	241					

RESULT	10
Q8S8Z0	
ID	PRELIMINARY; PRT; 319 AA.
AC	Q8S8Z0;
DT	01-JUN-2002 (T=EMBLrel. 21, Created)
DT	01-JUN-2002 (T=EMBLrel. 21, Last sequence update)
DT	01-OCT-2003 (T=EMBLrel. 25, Last annotation update)
DE	Protein phosphatase 2C.
MPC9.	
CN	Mesembryanthemum crystallinum (Common ice plant).
GN	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
CC	Caryophyllales; Aizoaceae; Mesembryanthemum.
CX	NCBI_TaxID=3544;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Miyazaki S., Izumi S., Fukuhara T., Bohnert H.J.;

"Plant Protein Phosphatases 2C ? A large protein family serving complex functions." ;

RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.

DR EMBL; AB083482; BAB8944.1; -

DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0000287; F:magnesium ion binding; IEA.

DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.

DR GO; GO:0006470; F:protein amino acid dephosphorylation; IEA.

DR InterPro; IPR000222; PP2C.

DR InterPro; IPR001932; PP2C-like.

DR Pfam; PF00481; PP2C; 1.

DR SMART; SM00332; PP2C; 1.

DR SMART; SM00331; PP2C_S1G; 1.

DR PROSITE; PS01032; PP2C; 1.

KW Hydrolase; Magnesium.

SQ SEQUENCE 319 AA; 34477 MW; 0BD228603E34CFB0 CRC64;

Query Match 20.2%; Score 408.5; DB 10; Length 319;

Best Local Similarity 39.6%; Pred. No. 1.3e-24;

Matches 113; Conservative 41; Mismatches 86; Indels 45; Gaps 12;

QY 109 GYVAERKGEREMQDAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNLIH 168

DB 35 GY-ASSPKRSSMEDFYETRIDVVG-----EVGLFGVFDGHHGIRAAEYVKQNL 85

QY 169 QNLIRKFKGDVISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKD-GSTATCVLAVDN 227

DB 86 SNLI-KHPK--FIS--DTKSAIAEAYHTDSEFLKSENTQN--RDAGSTASTAILVGD 136

QY 228 ILVIANLGDRAILCRYNESQKHAALSLSKEHNPTQYERMRICAKGNV---DGRVL 284

DB 137 RLLVANVGDSRAVICRGGE-----AIAVSRDHKPDQSDERQIEDAGGFVMAWGTWRVG 190

QY 285 GYLVSRISGDSQYKRCGVTSVPDIRRCOLTNDREIFILLACDGLFKVFTPEEAVNFILSC 344

DB 191 GYLVASRAFGDKLLKQY-VVADPEIQEEVDSLEFLILASDGLMDVVTNEEAVTMV--- 246

QY 345 LEDEKIQTRGKSAADARYEAACNLANKAVORGSDNVTVMVVR 389

DB 247 -----KPIQDT--EEAKLMQEAYQRGSDNITCVVR 278

RESULT 11

Q8RXV3 PRELIMINARY; PRT; 311 AA.

AC Q8RXV3; 21, Created

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN At4G31750.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCB_TaxID=3702;

[1]

SEQUENCE FROM N.A.

RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,

RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,

RA Carninci P., Chen H., Cheuk R., Hayaishizaki Y., Iehida J., Jones T.,

RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,

RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

RA Theologis A.

RT "Arabidopsis Full Length cDNA Clones." ;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.

RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hsuan V.W.,

RA Lee J.M., Quach H.L., Tang C., Toriumi M., Wu H.C., Yu G., Bowser L.,

RA

CArninci P., Chen H., Cheuk R., Hayaishizaki Y., Iehida J., Jones T.,

RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,

RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

RA Theologis A.

RT "Arabidopsis Open Reading Frame (ORF) Clones." ;

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.

DR EMBL; AY080658; AAL86334.1; -

DR EMBL; AY133761; AM91695.1; -

DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.

DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0000287; F:magnesium ion binding; IEA.

DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.

DR GO; GO:0006470; F:protein amino acid dephosphorylation; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR001993; Mitoch_carrier.

DR InterPro; IPR000222; PP2C.

DR InterPro; IPR001932; PP2C-like.

DR Pfam; PF00481; PP2C; 1.

DR PROSITE; PS00215; MITOCH_CARRIER; 1.

DR PROSITE; PS01032; PP2C; 1.

KW Hypothetical protein; Hydrolase; Magnesium.

SQ SEQUENCE 311 AA; 33247 MW; 5E3098B91F116BFD CRC64;

Query Match 19.7%; Score 398.5; DB 10; Length 311;

Best Local Similarity 39.3%; Pred. No. 7.7e-24;

Matches 112; Conservative 40; Mismatches 88; Indels 45; Gaps 12;

QY 109 GYVAERKGEREMQDAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNLIH 168

DB 35 GY-ASSPKRSSMEDFYETRIDVVG-----EVGLFGVFDGHHGIRAAEYVKQNL 85

QY 169 QNLIRKFKGDVISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKD-GSTATCVLAVDN 227

DB 86 SNLI-R-HPK--FIS--DTTAAIADAYNTDSEFLKSENSQN--RDAGSTASTAILVGD 136

QY 228 ILVIANLGDRAILCRYNESQKHAALSLSKEHNPTQYERMRICAKGNV---DGRVL 284

DB 137 RLLVANVGDSRAVICRGGN-----AIAVSRDHKPDQSDERQIEDAGGFVMAWGTWRVG 190

QY 285 GYLVSRISGDSQYKRCGVTSVPDIRRCOLTNDREIFILLACDGLFKVFTPEEAVNFILSC 344

DB 191 GYLVASRAFGDKLLKQY-VVADPEIQEEKVSLEFLILASDGLMDVVTNEEAVGMI-KA 248

QY 345 LEDEKIQTRGKSAADARYEAACNLANKAVORGSDNVTVMVVR 389

DB 249 IEDP-----EAGKRLMMEAYQRGSDNITCVVR 278

RESULT 12

Q7XR05 PRELIMINARY; PRT; 282 AA.

AC Q7XR05; 25, Created

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE OSUNBA0015K02.8 protein.

GN OSUNBA0015K02.8.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzoideae; Oryza.

OX NCB_TaxID=4530;

[1]

SEQUENCE FROM N.A.

RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,

RA Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,

RA Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,

RA Zhang Y., Hu H., Jia P.X., Qian Y.W., Ying K., Zhou B., Chen Z.H.,

RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,

RA Ren S.X., Lv G., Lin W., Gu W.O., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
RA Zhang Y., Cai Z., Chen J., Wang H., Chen X.Y., Shao C.Y., Sun Y.,
RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
RA Gu J.L., Chen S.T., Xi L., Zhu F.H., Hong G.F.,
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL606608; CA02891.1;
SQ SEQUENCE 282 AA; 30584 MW; B8FF3CF119534AB7 CRC64;

Query Match 19.4%; Score 391; DB 10; Length 282;
Best Local Similarity 36.7%; Pred. No. 2.7e-23;
Matches 106; Conservative 46; Mismatches 89; Indels 48; Gaps 9;

QY 109 GYVAERKGREREMQDAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASQAQNLH 168
DB 29 GY-ASPGKASMEFY-----ETRIDSVDGQIIGLVFGDGGAKVAEYVKQNL 79

QY 169 ONLIR--KPPKGDVISEVKTAKRLHQLNLR--KPPKGDVISEVKTAKRLHQLNLR 226
DB 80 SHLLRHPKFISTDVAID-----DAYKSTDSFLESDSSQNC---GSTASTAVLVG 128

QY 227 NLYLTANLGDRAILCRNYESQKHAALSKEHNPTQYERMIQKAGNVR---DGRV 283
DB 129 DSLFVANVGDSSRAIICRGNN-----AIAVSKDHKPKDQTDQRIEDAGGFVMMAGTWRV 182

QY 284 LGVLEVSRIQKAGNVR---DGRVIGVLEVSRIQKAGNVR---DGRVIGVLEVSRIQKAGNVR 343
DB 183 GGVLAVSRAFGKDLKQYVVD--PEIREVIDHSLDEFILASDGLDWDVVTNEEAVDMTRS 241

QY 344 CLEDEKIQITREKSAADARYAACNRLANKAVQSGADNVTVMVVRICH 392
DB 242 IHPDEE-----AAKLLQEAQYKRESSDNTICVVVRFLH 274

RESULT 13
Q8S3P1
ID Q8S3P1 PRELIMINARY; PRT; 243 AA.
AC Q8S3P1
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical protein.
GN 24K23.16.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Park Y.-J., Rostoks N., Ramakrishna W., SanMiguel P., Shiloff B.,
RA Ma J., Jiang Z., Kleinbols A., Bennetzen J.;
RT "Sequence characterization of orthologous regions in the barley and
RT rice genomes."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE P22C FAMILY.
DR EMBL; AF480497; AAL87187.1;
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0005498; F:binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR000222; P22C.
DR InterPro; IPR001932; P22C-like.
DR Pfam; PF00481; P22C; 1.
DR SMART; SM00332; P22C; 1.
DR SMART; SM00331; P22C; 1.
DR PROSITE; PS00215; MITOCH_CARRIER; 1.

DR PROSITE; PS01032; P22C; 1.
KW Hypothetical protein; Hydrolase; Magnesium.
SQ SEQUENCE 243 AA; 26734 MW; B8481E17F559CE5F CRC64;

Query Match 18.9%; Score 381.5; DB 10; Length 243;
Best Local Similarity 37.9%; Pred. No. 1.3e-22;
Matches 96; Conservative 43; Mismatches 75; Indels 39; Gaps 7;

QY 145 VYFAVFDGHHGIRASQAQNLHQLNLR--KPPKGDVISEVKTAKRLHQLNLR 202
DB 17 IGLFGVFDGHHGAKVAEYVKQNLHSHLLRHPKFISTDVAID-----DAYKSTDSF 68

QY 203 LKQASQKPAWKGSTATCVLAVNLIYANLGDRAILCRNYESQKHAALSKEHNPT 262
DB 69 LESDSQNC---GSTASTAVLVGDRLEFVANVGDSSRAIICRGNN-----AIAVSKDHK 119

QY 263 TQYERMIQKAGNVR---DGRVIGVLEVSRIQKAGNVR---DGRVIGVLEVSRIQKAGNVR 319
DB 120 DQTDQRIEDAGGFVMMAGTWRVGGVLAVSRAFGKDLKQYVVD--PEIREVIDHSL 178

QY 320 FILLACDGLFKVFTPEEAVNFILSCLEDEKIQITREKSAADARYAACNRLANKAVQSGS 379
DB 179 FILLASDGLDWDVVTNEEAVDMTRSIDHDEE-----AAKLLQEAQYKRES 222

QY 380 ADNVTVMVVRICH 392
DB 223 SDNITCVVVRFLH 235

RESULT 14
Q8LAY8
ID Q8LAY8 PRELIMINARY; PRT; 354 AA.
AC Q8LAY8
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein phosphatase 2C-like protein (Hypothetical protein).
GN AT5G10740/T30N20.10 OR AT5G10740.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volfovsky N., Town C.D., Troupkan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation."
RL Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troupkan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RT "Arabidopsis thaliana full-length cDNA."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;

"Arabidopsis Open Reading Frame (ORF) Clones";
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY087522; AAM65064.1; -;
DR EMBL; AK117549; BAC42210.1; -;
DR EMBL; BT0005431; AAO63851.1; -;
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004722; P:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C; 1.
DR PROSITE; PS00215; MITOCH_CARRIER; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hypothetical protein.
SQ SEQUENCE 354 AA; 38036 MW; 87DA535B561C9D68 CRC64;

Query Match 19.4%; Score 370.5; DB 10; Length 354;
Best Local Similarity 36.7%; Pred. No. 1.7e-21;
Matches 105; Conservative 47; Mismatches 87; Indels 47; Gaps 13;

QY 109 CYVAERKCEEMQD-AHVILNDITECRPSSLIITVSYFAVFDGHHGIRASKFAAQN 167
DB 35 GY-ASSAGKRSMDFFETRIDNGEI-----VGLFVFDGHHGARAAYVKRHL 84

QY 168 HQLIRKPKGDVLSVEKTVKRCILDTFKHTDEFLKQASSQKPAWK-DGSTATCVLAV 226
DB 85 FSNLI-THPK--FIS---DTKSAITDAYNHTDLSLKSNSHN---RDAGSTASTALVG 135

QY 227 NILYANLGDRAILCRYNESQKHAALSKEHNPTQYERMRIOKAGNVN---DGRV 283
DB 136 DRLVAVNGDSRAVISRGK-----AIASRDHKPDQSDERERENAGGVMMAGTWRV 189

QY 284 LGVLEVSISGGQYKRCVTSVPDIRRCOLTNDPFIACDGLFKVFTPEEAVNFILS 343
DB 190 GGVLAVSRAFGDRLKQY-VVADPEIQEKDDTLEFLILASDGLWDVFSNEAAVMV-- 246

QY 344 CLEDEKIQTRGKSAADARYEAACNRLANKAVQSGADNTVMVVR 369
DB 247 -----KEVEDP--EDSAKKLVGEAIKRGSDNITCVVVR 278

RESULT 15
QBVZD9 PRELIMINARY; PRT; 420 AA.
AC QBVZD9;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE AT553140/MFH8.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

[2]
SEQUENCE FROM N.A.
RP Cheuk R., Chen H., Kim C.J., Shinn P., Banh J., Bowser L.,
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis ORF clones";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
DR EMBL; AY085026; AAL57666.1; -;
DR EMBL; AY133656; AAM91486.1; -;
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; P:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium.
SQ SEQUENCE 420 AA; 45752 MW; 2DF6960D75BF9058 CRC64;

Query Match 18.3%; Score 368.5; DB 10; Length 420;
Best Local Similarity 32.8%; Pred. No. 3.1e-21;
Matches 112; Conservative 60; Mismatches 108; Indels 61; Gaps 13;

QY 64 TSISQVMTKTEGKAKRKTSEEEKNGSEELVEKKVKASSVIFGLK-----GVVAERK 115
DB 58 TSAKMWVDI-----SAGEKRISLVDMPPEKVDGGYIGGVKNDGSLSCGYCSFR- 108

QY 116 GREEMQDAHVILNDITECRPSSLIITVSYFAVFDGHHGIRASKFAAQNHLIRKF 175
DB 109 GKSTMEDFYDIKASTIEG-----QAVCMFGIFDGHGSSRAAEYLKHLFNLM-KH 159

QY 176 PKGDVISEKTVKRCILDTFKHTDEFLKQASSQKPAWK-DGSTATCVLAVNLYIANL 234
DB 160 PQ-----FLUTDKLALNETYKOTDVAFL-----SEKDTRDDGSTASAAVLGNHLYVANV 211

QY 235 GDSRAILCRYNESQKHAALSKEHNPTQYERMRIOKAGNVN---DGRVLGVLVSR 291
DB 212 GDSRTIV-----SKAGKAIASLDDHKPNRSDEKRIESAGGVIMWAGTWRVGGVLAMSR 265

QY 292 SIGDGOYKRCVTSVPDIRRCOLTNDPFIACDGLFKVFTPEEAVNFILSCLDEKIQ 351
DB 266 ALGNRLMKQF-VVABPEIQDLEIDHEALLVLSADGLWDVVDVFNEDAV--ALAAQSEEP-- 320

QY 352 TREGKSAADARYEAACNRLANKAVQSGADNTVMVVRIGH 392
DB 321 -----EAAARKLTDATFGRGSDNITCVVVRFRH 349

Search completed: April 12, 2004, 09:08:13
Job time : 48 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:00:56 ; Search time 58 seconds
(without alignments)
1909.631 Million cell updates/sec

Title: US-09-935-124A-2
Perfect score: 2018
Sequence: 1 MDLFGDLPERSPPRACK.....KAVQGSADNTVMVVRIGH 392

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Watch 0%
Maximum Watch 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:.*
1: Geneseq1980s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001s:.*
5: Geneseq2002s:.*
6: Geneseq2003as:.*
7: Geneseq2003bs:.*
8: Geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2018	100.0	392	AAB28791	Aab28791 Human hyd
2	2018	100.0	392	ABO5726	Abbo5726 Human sig
3	2018	100.0	392	ABG73740	Abg73740 Human ILK
4	2018	100.0	392	ADB30823	Adb30823 Human hyd
5	2018	100.0	392	ADE55482	Ades5482 Human Pro
6	2018	100.0	392	ADE55454	Ades5454 Human Pro
7	2018	100.0	392	ADE55466	Ades5466 Human Pro
8	2018	100.0	392	ADE55458	Ades5458 Human Pro
9	2018	100.0	421	ABBI2317	Abbi2317 Human pro
10	2018	100.0	421	AAH40555	Aam40555 Human pol
11	2018	100.0	441	AAU23566	Aau23566 Novel hum
12	2018	100.0	446	AAU22933	Aau22933 Novel hum
13	2015	99.9	392	AA32585	Aab32585 Human pro
14	2014	99.8	392	AA38769	Aam38769 Human pol
15	1931	95.7	392	ADE55484	Ades5484 Rat Prote
16	1931	95.7	392	ADE55452	Ades5452 Rat Prote
17	1931	95.7	392	ADE55456	Ades5456 Rat Prote
18	1931	95.7	392	ADE55460	Ades5460 Rat Prote
19	1927	95.5	392	ABP72390	Abp72390 Rat prote
20	1457.5	72.2	378	ABG09937	Abg09937 Novel hum
21	928	46.0	221	ABG09936	Abg09936 Novel hum
22	533.5	26.4	211	ABG07619	Abg07619 Novel hum
23	447.5	22.2	138	AAU23252	Aau23252 Novel hum
24	431.5	21.4	295	AA318068	Aag18068 Arabidops
25	431.5	21.4	305	AA318067	Aag18067 Arabidops

ALIGNMENTS

RESULT 1

AAB28791 ID AAB28791 standard; protein; 392 AA.

XX	AC	AAB28791;			
XX	DT	13-FEB-2001 (first entry)			
XX	DE	Human hydrolase-like molecule 2 protein.			
XX	KW	Hydrolase-like molecule; human; cell proliferation disorder; autoimmune;			
XX	KW	cancer; AIDS; acquired immune deficiency syndrome.			
XX	OS	Homo sapiens.			
XX	PN	US6132964-A.			
XX	PD	17-OCT-2000.			
XX	PF	06-FEB-1998; 98US-00013881.			
XX	PR	06-FEB-1998; 98US-00013881.			
XX	XX	(INCY-) INCYTE PHARM INC.			
XX	PA	Bandman O, Hillman JL, Guegler KJ, Shah P, Lal P, Corley NC;			
XX	PI	WPI; 2001-006133/01.			
XX	DR	N-PSDB; AAC60224.			
XX	PT	New human hydrolase-like molecules (HHLMs) and polynucleotides encoding the HHLMs, useful for diagnosing, treating or preventing cell proliferation (e.g. bone cancer) or autoimmune disorders(e.g. AIDS or asthma).			
XX	PS	Claim 1; Col 43-46; 38pp; English.			
XX	CC	The present invention relates to isolated and purified cDNA encoding a human hydrolase-like molecule (HHLM), designated HHLM-1 to HHLM-8. The HHLM DNAs and polypeptides are useful for diagnosing, treating or preventing cell proliferation disorders and autoimmune disorders. Cell proliferation disorders include cancers, autoimmune disorders include AIDS (acquired immune deficiency syndrome). The present sequence is a HHLM protein of the invention			
XX	SQ	Sequence 392 AA;			

Query Match 100.0%; Score 2018; DB 4; Length 392;

Aag03424 Human sec
Abb78060 Consensus
Aag18069 Arabidops
Abb77579 Physcomit
Abg74204 P. patens
Aag06997 Arabidops
Aag18039 Arabidops
Aag18039 Arabidops
Aag18039 Arabidops
Aag39774 Arabidops
Abb08198 Human-der
Acd89793 Human FEM
Aag39776 Arabidops
Aag18041 Arabidops
Aag18040 Arabidops
Aag39775 Arabidops
Aag06998 Arabidops
Abp56260 Herpicida
Abp56903 Arabidops
Abp56904 Arabidops
Abp56902 Arabidops

Best Local Similarity 100.0%; Pred. No. 4.8e-186;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLFGDLPEPERSPPAAGKEAQKGLPFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
DB 1 MDLFGDLPEPERSPPAAGKEAQKGLPFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
QY 61 SLATISQWVKTEGKAKRKTSEBEKNGSEBELVEKVKCKASSVIFGLKGYVAERKGEREE 120
DB 61 SLATISQWVKTEGKAKRKTSEBEKNGSEBELVEKVKCKASSVIFGLKGYVAERKGEREE 120
QY 121 MQDAHVLINDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180
DB 121 MQDAHVLINDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180
QY 181 ISVEKTVKRCCLDTFKHTDEBFLKQASSQKPAWKDGGSTATCVLAVDNILYIANLGSRAI 240
DB 181 ISVEKTVKRCCLDTFKHTDEBFLKQASSQKPAWKDGGSTATCVLAVDNILYIANLGSRAI 240
QY 241 LCRYNESQKHAALSLSKEHNPTQYEERMRQKAGGNVRDGRVGLVLEVSRSIGDQYKR 300
DB 241 LCRYNESQKHAALSLSKEHNPTQYEERMRQKAGGNVRDGRVGLVLEVSRSIGDQYKR 300
QY 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFTLSCLEDEKIQTRGKSAAD 360
DB 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFTLSCLEDEKIQTRGKSAAD 360
QY 361 ARYEACNRLANKAVQSGADNVTVMVRIGH 392
DB 361 ARYEACNRLANKAVQSGADNVTVMVRIGH 392

RESULT 2
ABB05726
ID ABB05726 standard; protein; 392 AA.
AC ABB05726;
XX 30-APR-2002 (first entry)
DE Human signal transduction protein clone tes3_j1j20.
KW Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
KW gene therapy.
OS Homo sapiens.
PN WO200198454-A2.
XX 27-DEC-2001.
XX 25-APR-2001; 2001WO-IB002050.
XX 25-APR-2000; 2000US-0199380P.
XX (GEHU-) GERMAN HUMAN GENOME PROJECT.
PA Wiemann S;
PI WPI; 2002-182647/18.
XX N-PSDB; ABQ77081.
XX Human cDNA sequences and clones derived from human fetal brain, fetal
XX kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
XX screening and therapy
XX English.
XX The present invention describes assemblies and computer readable media
XX comprising nucleic acid sequences and clones derived from human
XX cDNA libraries: foetal kidney, melanoma, testis and amygdala cDNA
XX libraries. AHA93702 to AHA93766 represent human cDNA sequences from the
XX present invention which encode the proteins given in ABB05662 to

CC ABB05729. The human cDNA sequences and clones can be used in gene
CC therapy. The clones may be used in a variety of applications, for example
CC they may be used in profiling assays, for providing large arrays of human
CC genetic material for implementing large-scale screening strategies and
CC for treating diseases via gene therapy procedures
XX
SQ Sequence 392 AA;
Query Match 100.0%; Score 2018; DB 5; Length 392;
Best Local Similarity 100.0%; Pred. No. 4.8e-186;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLFGDLPEPERSPPAAGKEAQKGLPFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
DB 1 MDLFGDLPEPERSPPAAGKEAQKGLPFDLPPASSTDSGGPGLLFDLPPASSGDSG 60
QY 61 SLATISQWVKTEGKAKRKTSEBEKNGSEBELVEKVKCKASSVIFGLKGYVAERKGEREE 120
DB 61 SLATISQWVKTEGKAKRKTSEBEKNGSEBELVEKVKCKASSVIFGLKGYVAERKGEREE 120
QY 121 MQDAHVLINDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180
DB 121 MQDAHVLINDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180
QY 181 ISVEKTVKRCCLDTFKHTDEBFLKQASSQKPAWKDGGSTATCVLAVDNILYIANLGSRAI 240
DB 181 ISVEKTVKRCCLDTFKHTDEBFLKQASSQKPAWKDGGSTATCVLAVDNILYIANLGSRAI 240
QY 241 LCRYNESQKHAALSLSKEHNPTQYEERMRQKAGGNVRDGRVGLVLEVSRSIGDQYKR 300
DB 241 LCRYNESQKHAALSLSKEHNPTQYEERMRQKAGGNVRDGRVGLVLEVSRSIGDQYKR 300
QY 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFTLSCLEDEKIQTRGKSAAD 360
DB 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFTLSCLEDEKIQTRGKSAAD 360
QY 361 ARYEACNRLANKAVQSGADNVTVMVRIGH 392
DB 361 ARYEACNRLANKAVQSGADNVTVMVRIGH 392

RESULT 3
ABB05740
ID ABB05740 standard; protein; 392 AA.
XX ABB05740;
AC ABB05740;
XX 27-MAR-2003 (first entry)
DE Human ILKAP protein.
XX ILKAP; integrin-linked kinase associated protein; Cl protein; human;
KW angiogenesis; modulator; cell surface marker expression; gene therapy;
KW avb3 integrin production; proliferation; differentiation.
OS Homo sapiens.
XX US2002156003-A1.
XX 24-OCT-2002.
XX 21-AUG-2001; 2001US-00935124.
XX 18-APR-2001; 2001US-0284760P.
XX (RIGE-) RIGEL PHARM INC.
XX Lorens JB, Xu W, Atchison RE, Bogenberger J;
XX WPI; 2003-182647/18.
XX N-PSDB; ABQ77081.
XX Identifying a compound that modulates angiogenesis, useful for monitoring

PT changes in cell surface marker expression or avb3 integrin production,
PT comprises contacting the compound with an integrin-linked kinase
XX associated protein.
XX
XX
XX Example 1; Fig 1; 20pp; English.
XX
XX This invention describes a novel compound that modulates angiogenesis
CC comprising contacting the compound with an integrin-linked kinase
CC associated protein (ILKAP) polypeptide, and determining the functional
CC effect of the compound on the ILKAP polypeptide. A method described in
CC the invention is useful for identifying modulators of angiogenesis, and
CC for monitoring changes in cell surface marker expression, avb3 integrin
CC production, proliferation and differentiation using either cell lines or
CC primary cells. The products of the invention can be used as ILKAP
CC modulators or for gene therapy. This sequence represents the human ILKAP
CC (also called C1 protein) describes in the disclosure of the invention
XX
XX Sequence 392 AA;
XX
XX Query Match 100.0%; Score 2018; DB 6; Length 392;
XX Best Local Similarity 100.0%; Pred. No. 4.8e-186;
XX Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLFGDLPEPERSPPRAAGKEAQKGLLFDLLPPASSTDSGSGPILLFDLLPPASGDSG 60
DB 1 MDLFGDLPEPERSPPRAAGKEAQKGLLFDLLPPASSTDSGSGPILLFDLLPPASGDSG 60
QY 61 SLATSIQMWKTEGKAKRTSEENKNGSEELVEKKVKCASSVIFGLKGYVAERKGEREE 120
DB 61 SLATSIQMWKTEGKAKRTSEENKNGSEELVEKKVKCASSVIFGLKGYVAERKGEREE 120
QY 121 MQDAHVLNDITECPSPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKPKGDV 180
DB 121 MQDAHVLNDITECPSPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKPKGDV 180
QY 181 ISVEKTVKRLDTPFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 240
DB 181 ISVEKTVKRLDTPFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 240
QY 241 LCRYNEESQKHAALSLSKEHNPTQYERNRIQAGGNVRDGRVLGVLEVSRSIGDQYKR 300
DB 241 LCRYNEESQKHAALSLSKEHNPTQYERNRIQAGGNVRDGRVLGVLEVSRSIGDQYKR 300
QY 301 CGVTSVPDIRRCQLTNPDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
DB 301 CGVTSVPDIRRCQLTNPDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
QY 361 ARYEAAACNRLANKAVQSGSADNVTVMVVRIGH 392
DB 361 ARYEAAACNRLANKAVQSGSADNVTVMVVRIGH 392

RESULT 4
ADB90823
ID ADB90823 standard; protein; 392 AA.
XX AC ADB90823;
XX DT 04-DEC-2003 (first entry)
XX DE Human hydrolase-like molecule, HMLM 2, INCYTE 195647.
XX KW Human; hydrolase-like molecule; HMLM; cell proliferation disorder;
XX KW arteriosclerosis; atherosclerosis; bursitis; psoriasis; cancer;
XX KW autoimmune disorder; AIDS; Addison's disease;
XX KW adult respiratory distress syndrome; anaemia; asthma; diabetes mellitus.
XX OS Homo sapiens.
XX PN US6518029-B1.
XX PD 11-FEB-2003.
XX

PF 07-JUL-2000; 2000US-00612473.
XX 06-FEB-1998; 98US-00013881.
XX (INCY-) INCYTE GENOMICS INC.
XX Bandman O, Lal P, Hillman JL, Corley NC, Guegler KJ, Shah P;
XX WPI; 2003-742789/70.
XX N-PSDB; ADB90831.
XX New human hydrolase-like molecules, useful for treating or preventing
XX cell proliferation disorders (e.g. atherosclerosis or cancers) and
XX autoimmune disorders (e.g. AIDS, Addison's disease, anemia, asthma and
XX diabetes mellitus).
XX Claim 1; Fig 2; 55pp; English.
XX The invention relates to a new isolated polypeptide comprising a human
XX hydrolase-like molecule, termed HMLM-8 appearing as ADB90822 - ADB90829,
XX a naturally occurring polypeptide comprising a sequence which is at least
XX 81% identical the HMLM, a biologically active fragment of an HMLM or an
XX immunogenic fragment comprising at least 15 contiguous amino acids. Also
XX included are a composition comprising an HMLM and an excipient, a method
XX for screening a compound as an agonist or antagonist of HMLM (by exposing
XX a sample comprising HMLM to a compound, and detecting agonist or
XX antagonist activity in the sample), a method for screening a compound
XX that specifically binds to HMLM (by combining HMLM with at least one test
XX compound, and detecting binding of HMLM to the test compound) and a
XX method for screening a compound that modulates the activity of HMLM. The
XX human hydrolase-like molecules (HMLM), agonists and antagonists useful
XX for treating or preventing cell proliferation disorders (e.g.
XX arteriosclerosis, atherosclerosis, bursitis, psoriasis, and cancers) and
XX autoimmune disorders (e.g. AIDS, Addison's disease, adult respiratory
XX distress syndrome, anaemia, asthma and diabetes mellitus). The HMLM
XX polypeptides are useful in preparing antibodies that specifically bind to
XX the polypeptides. Nucleic acids encoding HMLM are useful in generating
XX probes for mapping naturally occurring genomic sequences, in detecting
XX differences in the chromosomal location due to translocation or
XX inversion, and in screening libraries of compounds in drug screening
XX techniques. The present sequence represents an HMLM of the invention.
XX
XX Sequence 392 AA;
XX
XX Query Match 100.0%; Score 2018; DB 7; Length 392;
XX Best Local Similarity 100.0%; Pred. No. 4.8e-186;
XX Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLFGDLPEPERSPPRAAGKEAQKGLLFDLLPPASSTDSGSGPILLFDLLPPASGDSG 60
DB 1 MDLFGDLPEPERSPPRAAGKEAQKGLLFDLLPPASSTDSGSGPILLFDLLPPASGDSG 60
QY 61 SLATSIQMWKTEGKAKRTSEENKNGSEELVEKKVKCASSVIFGLKGYVAERKGEREE 120
DB 61 SLATSIQMWKTEGKAKRTSEENKNGSEELVEKKVKCASSVIFGLKGYVAERKGEREE 120
QY 121 MQDAHVLNDITECPSPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKPKGDV 180
DB 121 MQDAHVLNDITECPSPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKPKGDV 180
QY 181 ISVEKTVKRLDTPFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 240
DB 181 ISVEKTVKRLDTPFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 240
QY 241 LCRYNEESQKHAALSLSKEHNPTQYERNRIQAGGNVRDGRVLGVLEVSRSIGDQYKR 300
DB 241 LCRYNEESQKHAALSLSKEHNPTQYERNRIQAGGNVRDGRVLGVLEVSRSIGDQYKR 300
QY 301 CGVTSVPDIRRCQLTNPDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
DB 301 CGVTSVPDIRRCQLTNPDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
QY 361 ARYEAAACNRLANKAVQSGSADNVTVMVVRIGH 392

Query Match 100.0%; Score 2018; DB 7; Length 392;
Best Local Similarity 100.0%; Pred. No. 4.8e-186; Indels 0; Gaps 0;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPAAGKEAQKGLPDLPPASSTDSGGGGLPDLPPASSGDSG 60
DB 1 MDLFGDLPEPERSPPAAGKEAQKGLPDLPPASSTDSGGGGLPDLPPASSGDSG 60

QY 61 SLATISQMVKTGKAKRKTSEEEKNGSEELVEKKVKCKASSVIFGLKGYVAERKGEREE 120
DB 61 SLATISQMVKTGKAKRKTSEEEKNGSEELVEKKVKCKASSVIFGLKGYVAERKGEREE 120

QY 121 MQDAHVIINDITEECRPPSSLIIRVSYFAVFGHGGIRASKFAAQNHLNLRKFKPGDV 180
DB 121 MQDAHVIINDITEECRPPSSLIIRVSYFAVFGHGGIRASKFAAQNHLNLRKFKPGDV 180

QY 181 ISVEKTVKCLLDTFKHTEBEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGSRAI 240
DB 181 ISVEKTVKCLLDTFKHTEBEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGSRAI 240

QY 241 LCRYNEESQKHAALSLSKEHNPTQYEERNRIQKAGNVDRGVLGVLEVSRIQDQYKR 300
DB 241 LCRYNEESQKHAALSLSKEHNPTQYEERNRIQKAGNVDRGVLGVLEVSRIQDQYKR 300

QY 301 CGVTSVPDIRRQLTNDPDRFILLACDGLPKVTPPEAVNFILSCLEDEKIQTRKGSAD 360
DB 301 CGVTSVPDIRRQLTNDPDRFILLACDGLPKVTPPEAVNFILSCLEDEKIQTRKGSAD 360

QY 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
DB 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392

RESULT 6
ADE55454
ID ADE55454 standard; protein; 392 AA.
XX AC ADE55454;
XX DT 29-JAN-2004 (first entry)
XX DE Human Protein NP_110395, SEQ ID NO 1271.
XX KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
XX OS Homo sapiens.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX DR GENBANK; NP_110395.
XX PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017pp; English.
XX CC The invention discloses a composition comprising two or more isolated rat

DB 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392

RESULT 5
ADE55462
ID ADE55462 standard; protein; 392 AA.
XX AC ADE55462;
XX DT 29-JAN-2004 (first entry)
XX DE Human Protein NP_110395, SEQ ID NO 1279.
XX KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
XX OS Homo sapiens.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX DR GENBANK; NP_110395.
XX PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017pp; English.
XX CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX PS Sequence 392 AA;
XX CC

	Matches	392;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MDLFGDLPEPERSPPRAAGKAQGKPLLFDDLPASSTDSGSGPILLFDDLPPASSGDSC	60							
Db	1	MDLFGDLPEPERSPPRAAGKAQGKPLLFDDLPASSTDSGSGPILLFDDLPPASSGDSC	60							
Qy	61	STATSIQWVKTEGGAKRKTSSEKNGSELVEKKYCKASSVIFGLKGVAERKGEREE	120							
Db	61	STATSIQWVKTEGGAKRKTSSEKNGSELVEKKYCKASSVIFGLKGVAERKGEREE	120							
Qy	121	MQDAHVILNDITEECRPPSSITRVSPFAVPDGHGGIRASKFAAQNHLIRKPKGDV	180							
Db	121	MQDAHVILNDITEECRPPSSITRVSPFAVPDGHGGIRASKFAAQNHLIRKPKGDV	180							

QY 181 ISVEKTVKCLDTPKHTDEEFLKQASSQPAWKDGGSTATCVLAVDNILYIANLGDSPAI 240
 DB 181 ISVEKTVKCLDTPKHTDEEFLKQASSQPAWKDGGSTATCVLAVDNILYIANLGDSPAI 240
 QY 241 LCRYNEESQKHAALSLSKEHNPTQYEERMRIQKAGNVDGRVLGVLEVSRSIGDQYKR 300
 DB 241 LCRYNEESQKHAALSLSKEHNPTQYEERMRIQKAGNVDGRVLGVLEVSRSIGDQYKR 300
 QY 301 CGVTSVPDIRRCOLTPNDRFILLACDGLPKVFTPEEAVNFILSCLEDEKIQTRREGKSAAD 360
 DB 301 CGVTSVPDIRRCOLTPNDRFILLACDGLPKVFTPEEAVNFILSCLEDEKIQTRREGKSAAD 360
 QY 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
 DB 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392

RESULT 8
 ID ADE55458 standard; protein; 392 AA.
 AC ADE55458;
 XX 29-JAN-2004 (first entry)
 DT Human Protein NP_110395, SEQ ID NO 1275.
 DE Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 XX WC2003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 WPI; 2003-269312/26.
 DR GENBANK; NP_110395.

XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC the sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 392 AA;

Query Match 100.0%; Score 2018; DB 7; Length 392;
 Best Local Similarity 100.0%; Pred. No. 4.8e-186;
 Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDLFGDLPEPERSPRPAAGKEAQKGLLFDLPPASSTDSGGGPLLFDLPPASSGDSG 60
 DB 1 MDLFGDLPEPERSPRPAAGKEAQKGLLFDLPPASSTDSGGGPLLFDLPPASSGDSG 60
 QY 61 SLATSISQWVKTGKAGKKTSEEEKNGSEELVEKVKCKASSVIFGLKGVVAERKGEREE 120
 DB 61 SLATSISQWVKTGKAGKKTSEEEKNGSEELVEKVKCKASSVIFGLKGVVAERKGEREE 120
 QY 121 MQDAHVLNDITECRPPSSLIIRVSYPAVFDHGGIRASKFAAQNLHQLNLRKFPKGDV 180
 DB 121 MQDAHVLNDITECRPPSSLIIRVSYPAVFDHGGIRASKFAAQNLHQLNLRKFPKGDV 180
 QY 181 ISVEKTVKCLDTPKHTDEEFLKQASSQPAWKDGGSTATCVLAVDNILYIANLGDSPAI 240
 DB 181 ISVEKTVKCLDTPKHTDEEFLKQASSQPAWKDGGSTATCVLAVDNILYIANLGDSPAI 240
 QY 241 LCRYNEESQKHAALSLSKEHNPTQYEERMRIQKAGNVDGRVLGVLEVSRSIGDQYKR 300
 DB 241 LCRYNEESQKHAALSLSKEHNPTQYEERMRIQKAGNVDGRVLGVLEVSRSIGDQYKR 300
 QY 301 CGVTSVPDIRRCOLTPNDRFILLACDGLPKVFTPEEAVNFILSCLEDEKIQTRREGKSAAD 360
 DB 301 CGVTSVPDIRRCOLTPNDRFILLACDGLPKVFTPEEAVNFILSCLEDEKIQTRREGKSAAD 360
 QY 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
 DB 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392

RESULT 9
 ID ABB12317 standard; peptide; 421 AA.
 AC ABB12317;
 XX 11-JAN-2002 (first entry)

DE Human protein phosphatase 2C homologue, SEQ ID NO:2687.

XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnery; antiulcer.

OS Homo sapiens.

XX

PN WO200157186-A2.
 XX 09-AUG-2001.
 XX 05-FEB-2001; 2001WO-US003800.
 XX 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 PI WPI; 2001-457740/49.
 XX N-PSDB; ABA09561.
 DR Human proteins and DNA encoding sequences useful for preventing, treating
 PT and ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX Claim 20; Page 330; 1563pp; English.
 XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoietic regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 XX SQ Sequence 421 AA;
 Query Match 100.0%; Score 2018; DB 4; Length 421;
 Best Local Similarity 100.0%; Pred. No. 5.3e-186;
 Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDLFGDLPEPERSPPRPAAGKEAQKGLLFDLLPPASGTDGSGGGLLFDLLPPASGDSG 60
 DB 30 MDLFGDLPEPERSPPRPAAGKEAQKGLLFDLLPPASGTDGSGGGLLFDLLPPASGDSG 89
 QY 61 SLATISIQMVKTEGKGAKRTSEBEKNGSELVEKKVCKKASSVIFGLKGYVAERKEREE 120
 DB 90 SLATISIQMVKTEGKGAKRTSEBEKNGSELVEKKVCKKASSVIFGLKGYVAERKEREE 149

QY 121 MQDAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNLHQLIRKPKGDV 180
 DB 150 MQDAHVILNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNLHQLIRKPKGDV 209
 QY 181 ISVEKTVKRCLLDTFKETDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDRAI 240
 DB 210 ISVEKTVKRCLLDTFKETDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDRAI 269
 QY 241 LCRYNEESQKHAALSLSKEHNPTQYEEEMRIQKAGNVDRGVGLVLEVSRSIGDQYKR 300
 DB 270 LCRYNEESQKHAALSLSKEHNPTQYEEEMRIQKAGNVDRGVGLVLEVSRSIGDQYKR 329
 QY 301 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRREGKSAAD 360
 DB 330 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRREGKSAAD 389
 QY 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392
 DB 390 ARYEACNRLANKAVQSGADNVTVMVVRIGH 421
 RESULT 10
 AAM40555
 ID AAM40555 standard; protein; 421 AA.
 XX AC AAM40555;
 XX 22-OCT-2001 (first entry)
 DE Human polypeptide SEQ ID NO 5486.
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX OS Homo sapiens.
 XX WO200153312-A1.
 XX 26-JUL-2001.
 PD 26-DEC-2000; 2000WO-US034263.
 PF 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 DR WPI; 2001-442253/47.
 DR N-PSDB; AAI59711.
 XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 XX Example 2; SEQ ID NO 5486; 10078pp; English.
 XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAM38642-AAM42213) with nootropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX

SQ Sequence 421 AA;

Query Match 100.0%; Score 2018; DB 4; Length 421;
Best Local Similarity 100.0%; Pred. No. 5.3e-186;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFDLPEPERSPPRAAGKEAQKGLFLFDLPASSTDSGGPFLFDLPASSGDSG 60
DB 30 MDLFDLPEPERSPPRAAGKEAQKGLFLFDLPASSTDSGGPFLFDLPASSGDSG 89
QY 61 SLATISQWVTEGKAKKTSSEBKNGSELVEKKVCKASSVIFGLKGYVAERKGEREE 120
DB 90 SLATISQWVTEGKAKKTSSEBKNGSELVEKKVCKASSVIFGLKGYVAERKGEREE 149
QY 121 MQDAVIINDITEECRPSSIIITVSYFAVFDGHHGIRPASKFAAQNLHONLIRFKPGDV 180
DB 150 MQDAVIINDITEECRPSSIIITVSYFAVFDGHHGIRPASKFAAQNLHONLIRFKPGDV 209
QY 181 ISVEKTVKRCLLDTFKHDEEFLKQASSQKPAWKDGGTATCVLAVDNILYITANIGDSRAI 240
DB 210 ISVEKTVKRCLLDTFKHDEEFLKQASSQKPAWKDGGTATCVLAVDNILYITANIGDSRAI 269
QY 241 LCRNEESQKHAALSLSKEHNPQYEEEMRIQKAGGNVDRGVLGVLEVSRSIGDGYKR 300
DB 270 LCRNEESQKHAALSLSKEHNPQYEEEMRIQKAGGNVDRGVLGVLEVSRSIGDGYKR 329
QY 301 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRREGKSAAD 360
DB 330 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRREGKSAAD 389
QY 361 ARYEAAACNRLANKAVQGSADNTVMVVRIGH 392
DB 390 ARYEAAACNRLANKAVQGSADNTVMVVRIGH 421

RESULT 11

AAU23566
ID AAU23566 standard; protein; 441 AA.

XX AC AAU23566;

XX DT 17-DEC-2001 (first entry)

XX DE Novel human enzyme polypeptide #652.

XX KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
XX ligase; hyperproliferative disorder; immunodeficiency disorder;
XX autoimmune disorder; neurological disorder; metabolic disorder;
XX inflammatory disorder; cardiovascular disorder; reproductive disorder;
XX blood-related disorder; infectious disorder; cytostatic; anti arthritic;
XX nephrotropic; anticoagulant.

OS Homo sapiens.

XX PN WO20015301-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US001239.

XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 15-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-020515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 14-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.

02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0246167P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251388P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
FA Rosen CA, Barash SC, Ruben SM;
XX WPT; 2001-465566/50.
XX N-PSDB; AAS41435.
XX Novel polypeptides and polynucleotides useful for diagnosing, preventing,

PT treating neural, immune system, muscular, reproductive, pulmonary,
PT cardiovascular, renal, proliferative disorders and cancerous diseases.
XX Claim 11; SEQ ID NO 1562; 1180pp; English.
XX The present invention relates to the isolation of novel human enzyme
CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC infectious disorders (e.g. Influenza). The polynucleotides of the
CC invention can also be used in gene therapy. AAU22915-AAU23814 represent
CC the novel human enzyme polypeptides of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 441 AA;

Query Match 100.0%; Score 2018; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. NO. 5.7e-186;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLFGDLPEPERSPPAAKGAKEAKGKPLLFDDLPASSTDSGGGPIILFDDLPASSGDSG 60
Db 50 MDLFGDLPEPERSPPAAKGAKEAKGKPLLFDDLPASSTDSGGGPIILFDDLPASSGDSG 109
QY 61 SLATSIQVMKTECKGAKRKTSEEEKNGSBEKVKYCKASSVIFGLKGYVAERKGEREE 120
Db 110 SLATSIQVMKTECKGAKRKTSEEEKNGSBEKVKYCKASSVIFGLKGYVAERKGEREE 169
QY 121 MQDAHVILNDITECRPPSSLIIRVSYFAVFDGHHGIRASKFAAQNHLIRKPKGDV 180
Db 170 MQDAHVILNDITECRPPSSLIIRVSYFAVFDGHHGIRASKFAAQNHLIRKPKGDV 229
QY 181 ISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNLIYANLGDRAI 240
Db 230 ISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNLIYANLGDRAI 289
QY 241 LCRYNESQKHAALSLSKEHNPTQYERMRIQKAGNVRDGRVLGVLEVSISDGGYKR 300
Db 290 LCRYNESQKHAALSLSKEHNPTQYERMRIQKAGNVRDGRVLGVLEVSISDGGYKR 349
QY 301 CGVTSVPDIRCQLTPNDRPILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRREGKSAAD 360
Db 350 CGVTSVPDIRCQLTPNDRPILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRREGKSAAD 409
QY 361 ARYEAAACNRLANKAVQGSADNTVMVVRIGH 392
Db 410 ARYEAAACNRLANKAVQGSADNTVMVVRIGH 441

RESULT 12
AAU22933
ID AAU22933 standard; protein; 446 AA.
XX AC AAU22933;
XX 17-DEC-2001 (first entry)
XX Novel human enzyme polypeptide #19.
XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;

KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX Homo sapiens.
OS WO200155301-A2.
PN 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US001239.
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0190628P.
PR 24-FEB-2000; 2000US-0184564P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190763P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216847P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228242P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 11-OCT-2000; 2000US-0239935P.
PR 11-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0244674P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246603P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0251479P.
PR 06-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.

PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI: 2001-465566/50.
XX N-PSDB; AAS40803.
XX Novel polypeptides and polynucleotides useful for diagnosing, preventing,
PT treating neural, immune system, muscular, reproductive, pulmonary,
PT cardiovascular, renal, proliferative disorders and cancerous diseases.
XX
XX Claim 11; SEQ ID NO 929; 1180pp; English.
XX
XX The present invention relates to the isolation of novel human enzyme
CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic
CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),
CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders
CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and
CC infectious disorders (e.g. Influenza). The polynucleotides of the
CC invention can also be used in gene therapy. AAU22915-AAU23814 represent
CC the novel human enzyme polypeptides of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 446 AA;
XX
Query Match 100.0%; Score 2018; DB 4; Length 446;
Best Local Similarity 100.0%; Pred. No. 5.8e-186;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDLFGDLPEPERSPPRPAAGKEAQKGPLLFDLPPASSTDSGGPGLLFDLPPASGDSG 60
Db 55 MDLFGDLPEPERSPPRPAAGKEAQKGPLLFDLPPASSTDSGGPGLLFDLPPASGDSG 114
Qy 61 SLATSISQVMTKTEGKAKRTSEEEKNGSELVEKVKYKASSVIFGLKGYVAERKGEREE 120
Db 115 SLATSISQVMTKTEGKAKRTSEEEKNGSELVEKVKYKASSVIFGLKGYVAERKGEREE 174
Qy 121 MCDARVILNDITECRPPSSLITRVSYFAVFDGHHGIRASGKFAAQNHLIRKPKGDV 180
Db 175 MCDARVILNDITECRPPSSLITRVSYFAVFDGHHGIRASGKFAAQNHLIRKPKGDV 234
Qy 181 ISVEKTVKRCLLDTFKHTDEEFLQAASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 240
Db 235 ISVEKTVKRCLLDTFKHTDEEFLQAASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 294
Qy 241 LCRYNEESQKHAALSLSKEHNPTQYERMRITQKAGNVDRGVLGVLVRSRIGDGGYKR 300
Db 295 LCRYNEESQKHAALSLSKEHNPTQYERMRITQKAGNVDRGVLGVLVRSRIGDGGYKR 354
Qy 301 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKICTREGKSAAD 360
Db 355 CGVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKICTREGKSAAD 414
Qy 361 ARYEAAACNRLANKAVORGADNVTVVVRIGH 392
Db 415 ARYEAAACNRLANKAVORGADNVTVVVRIGH 446

AAB92585;
XX 26-JUN-2001 (first entry)
XX Human protein sequence SEQ ID NO:10816.
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX Homo sapiens.
XX EP1074617-A2.
XX 07-FEB-2001.
XX 28-JUL-2000; 2000EP-00116126.
XX 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX (HELI-) HELIX RES INST.
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI: 2001-318749/34.
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
XX Claim 8; SEQ ID NO 10816; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dr primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
XX Sequence 392 AA;
XX
Query Match 99.9%; Score 2015; DB 4; Length 392;
Best Local Similarity 99.7%; Pred. No. 9.3e-186;
Matches 391; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDLFGDLPEPERSPPRPAAGKEAQKGPLLFDLPPASSTDSGGPGLLFDLPPASGDSG 60
Db 1 MDLFGDLPEPERSPPRPAAGKEAQKGPLLFDLPPASSTDSGGPGLLFDLPPASGDSG 60
Qy 61 SLATSISQVMTKTEGKAKRTSEEEKNGSELVEKVKYKASSVIFGLKGYVAERKGEREE 120
Db 61 SLATSISQVMTKTEGKAKRTSEEEKNGSELVEKVKYKASSVIFGLKGYVAERKGEREE 120

QY	121	MODAHVILNDITECRPPSSLI	TRVSYFAVFDGGHGI	RASKFAAQNLHONLIRKPPKGDV	180
Db	121	MODAHVILNDITECRPPSSLI	TRVSYFAVFDGGHGI	RASKFAAQNLHONLIRKPPKGDV	180
QY	181	ISVEKTVKRCCLDTFKHTDE	EFKQASSQKPAWKD	STATCVLAVDNILYIANLGDSRAI	240
Db	181	ISVEKTVKRCCLDTFKHTDE	EFKQASSQKPAWKD	STATCVLAVDNILYIANLGDSRAI	240
QY	241	LCRYNEESQKHAALSLSKEH	NPTQYEERMRIOKAGN	VRDGRVLGVLEVSRSIGDGOYKR	300
Db	241	LCRYNEESQKHAALSLSKEH	NPTQYEERMRIOKAGN	VRDGRVLGVLEVSRSIGDGOYKR	300
QY	301	CGVTSVPDIRRCQLT	PNDRFILLACDGLFKVFT	PEEAVNFILSCLEDEKIQTRGKSAAD	360
Db	301	CGVTSVPDIRRCQLT	PNDRFILLACDGLFKVFT	PEEAVNFILSCLEDEKIQTRGKSAAD	360
QY	361	ARYEAAACNRLANKAVOR	GSADNVTVVVRIGH	392	
Db	361	ARYEAAACNRLANKAVOR	GSADNVTVVVRIGH	392	
RESULT 14					
AM38769					
ID	AA38769	standard; protein; 392 AA.			
XX					
AC	AA38769;				
XX					
DT	22-OCT-2001	(first entry)			
DE					
XX					
XX					
KW	Human; nototropic; immunosuppressant; cytostatic; gene therapy; cancer;				
KW	peripheral nervous system; neuropathy; central nervous system; CNS;				
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;				
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;				
KW	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;				
KW	leukaemia.				
OS	Homo sapiens.				
XX					
PN	WO200153312-A1.				
XX					
PD	26-JUL-2001.				
XX					
PF	26-DEC-2000; 2000WO-US034263.				
XX					
PR	23-DEC-1999; 99US-00471275.				
PR	21-JAN-2000; 2000US-00488725.				
PR	25-APR-2000; 2000US-00552317.				
PR	20-JUN-2000; 2000US-00598042.				
PR	19-JUL-2000; 2000US-00620312.				
PR	03-AUG-2000; 2000US-00653450.				
PR	14-SEP-2000; 2000US-00662191.				
PR	19-OCT-2000; 2000US-00693036.				
PR	29-NOV-2000; 2000US-00727344.				
XX					
PA	(HYSE-) HYSEQ INC.				
XX					
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;				
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;				
PI	Zhou P, Goodrich R, Drmanac RT;				
XX					
DR	WPI: 2001-442253/47.				
DR	N-PSDB; AA157925.				
XX					
PT	Novel nucleic acids and polypeptides, useful for treating disorders such				
PT	as central nervous system injuries.				
XX					
PS	Example 3; SEQ ID NO 1914; 10078pp; English.				
XX					
CC	The invention relates to human nucleic acids (AA157799-AA161369) and the				
CC	encoded polypeptides (AA38642-AA42213) with nootropic,				
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful				
CC					

CC	in gene therapy. A composition containing a polypeptide or polynucleotide				
CC	of the invention may be used to treat diseases of the peripheral nervous				
CC	system, such as peripheral nervous injuries, peripheral neuropathy and				
CC	localised neuropathies and central nervous system diseases, such as				
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic				
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the				
CC	utilisation of the activities such as: Immune system suppression,				
CC	Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic				
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,				
CC	assays for receptor activity, arthritis and inflammation, leukaemias and				
CC	C.N.S disorders. Note: The sequence data for this patent did not form				
CC	part of the printed specification				
XX					
SQ	Sequence 392 AA;				
Query Match 99.8%; Score 2014; DB 4; Length 392;					
Best Local Similarity 99.7%; Pred. No. 1.2e-185;					
Matches 391; Conservative 1; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MDLFGDLPEPERSPRPAAGKEA	QKGPLLFDLPPASS	TDSSGGPLLPDLPPASSGDSG	60
Db	1	MDLFGDLPEPERSPRPAAGKEA	QKGPLLFDLPPASS	TDSSGGPLLPDLPPASSGDSG	60
QY	61	SLATSISQMVKTGEGAKRKTSE	EEKNGSEELVEKVKCKASSVI	FGLKGYVAERKGEREE	120
Db	61	SLATSISQMVKTGEGAKRKTSE	EEKNGSEELVEKVKCKASSVI	FGLKGYVAERKGEREE	120
QY	121	MODAHVILNDITECRPPSSLI	TRVSYFAVFDGGHGI	RASKFAAQNLHONLIRKPPKGDV	180
Db	121	MODAHVILNDITECRPPSSLI	TRVSYFAVFDGGHGI	RASKFAAQNLHONLIRKPPKGDV	180
QY	181	ISVEKTVKRCCLDTFKHTDE	EFKQASSQKPAWKD	STATCVLAVDNILYIANLGDSRAI	240
Db	181	ISVEKTVKRCCLDTFKHTDE	EFKQASSQKPAWKD	STATCVLAVDNILYIANLGDSRAI	240
QY	241	LCRYNEESQKHAALSLSKEH	NPTQYEERMRIOKAGN	VRDGRVLGVLEVSRSIGDGOYKR	300
Db	241	LCRYNEESQKHAALSLSKEH	NPTQYEERMRIOKAGN	VRDGRVLGVLEVSRSIGDGOYKR	300
QY	301	CGVTSVPDIRRCQLT	PNDRFILLACDGLFKVFT	PEEAVNFILSCLEDEKIQTRGKSAAD	360
Db	301	CGVTSVPDIRRCQLT	PNDRFILLACDGLFKVFT	PEEAVNFILSCLEDEKIQTRGKSAAD	360
QY	361	ARYEAAACNRLANKAVOR	GSADNVTVVVRIGH	392	
Db	361	ARYEAAACNRLANKAVOR	GSADNVTVVVRIGH	392	
RESULT 15					
ADE55464					
ID	ADE55464	standard; protein; 392 AA.			
XX					
AC	ADE55464;				
XX					
DT	29-JAN-2004	(first entry)			
XX					
DE					
XX					
XX					
KW	Rat Protein AAC97497, SEQ ID NO 1281.				
KW	Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;				
KW	chronic constriction injury; CCI; spared nerve injury; SNI; Chung.				
OS	Rattus norvegicus.				
XX					
PN	WO2003016475-A2.				
XX					
PD	27-FEB-2003.				
XX					
PF	14-AUG-2002; 2002WO-US025765.				
XX					
PR	14-AUG-2001; 2001US-0312147P.				
PR	01-NOV-2001; 2001US-0346382P.				
PR	26-NOV-2001; 2001US-0333347P.				
XX					

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:07:23 ; Search time 46 Seconds
(without alignments)

2240.689 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 2018

Sequence: 1 MDLFGDLPEPERSPPRAAGK.....KAVQGSADNVTVVVRIGH 392

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2018	100.0	392	9	US-09-935-124A-2
2	2018	100.0	392	14	US-10-359-499-2
3	2018	100.0	421	12	US-10-276-774-2697
4	1927	95.5	392	14	US-10-218-137-22
5	1277	63.3	248	14	US-10-147-874-3
6	422.5	20.9	260	12	US-10-072-012-853
7	421.5	20.9	300	14	US-10-170-789-35
8	403.5	20.0	252	12	US-10-072-012-854
9	403.5	20.0	338	12	US-10-424-599-226401
10	403.5	20.0	338	12	US-10-424-599-226412
11	399.5	19.8	314	12	US-10-424-599-219869
12	397.5	19.7	312	12	US-10-424-599-219880
13	395.5	19.6	274	9	US-09-860-351-4
14	388	19.2	371	12	US-10-425-114-66152
15	386	19.1	333	12	US-10-425-114-62620

16	374	18.5	310	12	US-10-425-114-50324	Sequence 50324, A
17	374	18.5	310	12	US-10-425-114-60282	Sequence 60282, A
18	373	18.5	310	12	US-10-425-114-46846	Sequence 46846, A
19	371.5	18.4	416	12	US-10-425-114-59347	Sequence 59347, A
20	370.5	18.4	353	9	US-09-828-302-14	Sequence 14, Appl
21	369.5	18.3	416	12	US-10-425-114-72766	Sequence 72766, A
22	362.5	18.0	334	12	US-10-425-114-63384	Sequence 63384, A
23	362.5	18.0	343	12	US-10-425-114-67289	Sequence 67289, A
24	359.5	17.8	379	12	US-10-425-114-55704	Sequence 55704, A
25	358.5	17.8	345	12	US-10-425-114-65340	Sequence 65340, A
26	358.5	17.8	361	14	US-10-178-977A-2	Sequence 2, Appl
27	358.5	17.8	361	14	US-10-178-977A-4	Sequence 4, Appl
28	358.5	17.7	361	14	US-10-178-977A-6	Sequence 6, Appl
29	356.5	17.7	356	12	US-10-425-114-39847	Sequence 39847, A
30	354	17.5	356	12	US-10-424-599-208454	Sequence 208454, A
31	353.5	17.5	434	14	US-10-171-404A-46	Sequence 46, Appl
32	353.5	17.5	438	12	US-09-816-277-10	Sequence 10, Appl
33	353	17.5	383	12	US-10-424-599-191145	Sequence 191145, A
34	353	17.5	400	12	US-10-425-114-46211	Sequence 46211, A
35	352.5	17.5	370	12	US-10-425-114-69654	Sequence 69654, A
36	352.5	17.5	375	12	US-10-425-114-63857	Sequence 63857, A
37	352	17.4	482	12	US-10-425-114-58868	Sequence 58868, A
38	350	17.3	339	12	US-10-425-114-43779	Sequence 43779, A
39	349.5	17.3	360	12	US-10-425-114-70158	Sequence 70158, A
40	348.5	17.3	455	15	US-10-108-260A-4628	Sequence 4628, Ap
41	348	17.2	370	15	US-10-369-493-22760	Sequence 22760, A
42	347.5	17.2	528	12	US-10-425-114-40731	Sequence 40731, A
43	347.5	17.2	595	12	US-10-424-599-248091	Sequence 248091, A
44	347	17.2	348	15	US-10-369-493-5704	Sequence 5704, Ap
45	346.5	17.2	396	12	US-10-425-114-58998	Sequence 58998, A

ALIGNMENTS

RESULT 1

US-09-935-124A-2

; Sequence 2, Application US/09935124A

; Patent No. US20020156003A1

; GENERAL INFORMATION:

; APPLICANT: Lorens, James

; APPLICANT: Xu, Weiduan

; APPLICANT: Atchison, Robert

; APPLICANT: Bogenberger, Jakob

; TITLE OF INVENTION: Modulators of Angiogenesis

; FILE REFERENCE: 021044-000210us

; CURRENT APPLICATION NUMBER: US/09/935,124A

; CURRENT FILING DATE: 2002-05-21

; PRIOR APPLICATION NUMBER: 60/284,760

; PRIOR FILING DATE: 2001-04-16

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 2

; LENGTH: 392

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-935-124A-2

Query Match 100.0%; Score 2018; DB 9; Length 392;
Best Local Similarity 100.0%; Pred. No. 3.1e-181;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDLFGDLPEPERSPPRAAGKQAQKGLFDLLPPASSTDSGGPGLFDLLPPASGGSG	60
DB	1	MDLFGDLPEPERSPPRAAGKQAQKGLFDLLPPASSTDSGGPGLFDLLPPASGGSG	60
QY	61	SLATSISQWVTEGAKRKTSEEEKNGSEELVEKKVCASSVIFGLGYVAERKGEREE	120
DB	61	SLATSISQWVTEGAKRKTSEEEKNGSEELVEKKVCASSVIFGLGYVAERKGEREE	120
QY	121	MODAHVILNDITECRPPSSLIITRVSFAVFDGHGIRASKFAAQNHLIRKPKGDV	180
DB	121	MODAHVILNDITECRPPSSLIITRVSFAVFDGHGIRASKFAAQNHLIRKPKGDV	180

QY 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGGSTATCVLAVDNILYIANLGDRAI 240
 Db 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGGSTATCVLAVDNILYIANLGDRAI 240
 QY 241 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVRDGRVLGVLEVSRSIGDQYKR 300
 Db 241 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVRDGRVLGVLEVSRSIGDQYKR 300
 QY 301 CGVTSVPDIRRRCQLTPNDRFILLACDGLFKVFTPEAVNFILSCLEDEKIQTRGKSAAD 360
 Db 301 CGVTSVPDIRRRCQLTPNDRFILLACDGLFKVFTPEAVNFILSCLEDEKIQTRGKSAAD 360
 QY 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
 Db 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392

RESULT 2

US-10-359-499-2
 ; Sequence 2, Application US/10359499
 ; Publication No. US20030148363A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
 ; FILE REFERENCE: PF-0470-1 CIP
 ; CURRENT APPLICATION NUMBER: US/10/359,499
 ; CURRENT FILING DATE: 2003-02-05
 ; PRIOR APPLICATION NUMBER: US/09/612,473
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: 09/013,881
 ; PRIOR FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 55
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 2
 ; LENGTH: 392
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030148363A1 195647
 US-10-359-499-2

Query Match 100.0%; Score 2018; DB 14; Length 392;
 Best Local Similarity 100.0%; Pred. No. 3.1e-181;
 Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPAAGKEAQKGLLFDLLPPASSTDSGGGPLLFDLLPPASSGDSG 60
 Db 1 MDLFGDLPEPERSPPAAGKEAQKGLLFDLLPPASSTDSGGGPLLFDLLPPASSGDSG 60
 QY 61 SLATSIQMVKTGKAKRTSEEEKNGSEELVEKVKCASSVIFGLKGYVAERKGEREE 120
 Db 61 SLATSIQMVKTGKAKRTSEEEKNGSEELVEKVKCASSVIFGLKGYVAERKGEREE 120
 QY 121 MQDAHVLNDITEECRPSSLLITRVSFAVFDGHHGIRASKFAAQNHLNLRKFPKGDV 180
 Db 121 MQDAHVLNDITEECRPSSLLITRVSFAVFDGHHGIRASKFAAQNHLNLRKFPKGDV 180
 QY 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGGSTATCVLAVDNILYIANLGDRAI 240
 Db 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGGSTATCVLAVDNILYIANLGDRAI 240
 QY 241 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVRDGRVLGVLEVSRSIGDQYKR 300
 Db 241 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVRDGRVLGVLEVSRSIGDQYKR 300
 QY 301 CGVTSVPDIRRRCQLTPNDRFILLACDGLFKVFTPEAVNFILSCLEDEKIQTRGKSAAD 360

Db 301 CGVTSVPDIRRRCQLTPNDRFILLACDGLFKVFTPEAVNFILSCLEDEKIQTRGKSAAD 360
 QY 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
 Db 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392

RESULT 3

US-10-276-774-2687
 ; Sequence 2687, Application US/10276774
 ; Publication No. US20040053245A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; APPLICANT: Tang, Y, Tom et al
 ; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
 ; FILE REFERENCE: 21272-030
 ; CURRENT APPLICATION NUMBER: US/10/276,774
 ; CURRENT FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: 09/560,875
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: 09/496,914
 ; PRIOR FILING DATE: 2000-02-03
 ; NUMBER OF SEQ ID NOS: 2700
 ; SOFTWARE: Custom
 ; SEQ ID NO 2687
 ; LENGTH: 421
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-276-774-2687

Query Match 100.0%; Score 2018; DB 12; Length 421;
 Best Local Similarity 100.0%; Pred. No. 3.4e-181;
 Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPAAGKEAQKGLLFDLLPPASSTDSGGGPLLFDLLPPASSGDSG 60
 Db 30 MDLFGDLPEPERSPPAAGKEAQKGLLFDLLPPASSTDSGGGPLLFDLLPPASSGDSG 89
 QY 61 SLATSIQMVKTGKAKRTSEEEKNGSEELVEKVKCASSVIFGLKGYVAERKGEREE 120
 Db 90 SLATSIQMVKTGKAKRTSEEEKNGSEELVEKVKCASSVIFGLKGYVAERKGEREE 149
 QY 121 MQDAHVLNDITEECRPSSLLITRVSFAVFDGHHGIRASKFAAQNHLNLRKFPKGDV 180
 Db 150 MQDAHVLNDITEECRPSSLLITRVSFAVFDGHHGIRASKFAAQNHLNLRKFPKGDV 209
 QY 181 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGGSTATCVLAVDNILYIANLGDRAI 240
 Db 210 ISVEKTVKRCCLDTPFKHTDEEFLKQASSQKPAWKDGGSTATCVLAVDNILYIANLGDRAI 269
 QY 241 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVRDGRVLGVLEVSRSIGDQYKR 300
 Db 270 LCRYNESQKHAALSLSKEHNPTQYERMRIOKAGNVRDGRVLGVLEVSRSIGDQYKR 329
 QY 301 CGVTSVPDIRRRCQLTPNDRFILLACDGLFKVFTPEAVNFILSCLEDEKIQTRGKSAAD 360
 Db 330 CGVTSVPDIRRRCQLTPNDRFILLACDGLFKVFTPEAVNFILSCLEDEKIQTRGKSAAD 389
 QY 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
 Db 390 ARYEACNRLANKAVQSGADNVTVVVRIGH 421

RESULT 4

US-10-218-137-22
 ; Sequence 22, Application US/10218137
 ; Publication No. US20030171255A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Greengard, Paul
 ; APPLICANT: Svenningsson, Per
 ; APPLICANT: Rakhilin, Sergey
 ; APPLICANT: Starkova, Natalia

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATION OF DARPP-32 PHOSPHORYLATION
; FILE REFERENCE: 11181-005
; CURRENT APPLICATION NUMBER: US/10/218,137
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 60/311,641
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 22
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-218-137-22

Query Match 95.5%; Score 1927; DB 14; Length 392;
Best Local Similarity 94.9%; Pred. No. 1.2e-172;
Matches 372; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRPAAGKEAQKPLLFDDLPASSSTDGSGGPGPLFFDLPASSGDSG 60
DB 1 MDLFGDLPEPERAPRPSAGKEAQKPLFFEDLPSTSDSGSGGPGPLFFDLPAGSGNSG 60

QY 61 SLATISQMVTEGKAKRTSEKNGSBEKVKCKKASSVIFGLKGVVAERKGEREE 120
DB 61 SLATSGSQVKNEGKAKRKAPBEDNGGBELVEKVKCKKASSVIFGLKGVVAERKGEREE 120

QY 121 MODAHVILNDITECRPPSSLIITVSVYFAVFDGGHGGIRASKFAAQNHLIRKFKGVDV 180
DB 121 MODAHVILNDITQCNPPSSLIITVSVYFAVFDGGHGGIRASKFAAQNHLIRKFKGVDV 180

QY 181 ISVEKTVKRCLLDTFKHTDEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDSPRAI 240
DB 181 ISVEKTVKRCLLDTFKHTDEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDSPRAI 240

QY 241 LCRYNEESQKHAALSLSKEHNFTQYEEEMRIQKAGNVDRGVLGVLEVSRSIGDQYKR 300
DB 241 LCRYNEESQKHAALSLSKEHNFTQYEEEMRIQKAGNVDRGVLGVLEVSRSIGDQYKR 300

QY 301 CGVTSVPDIRCQLTNPNDRIILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAAD 360
DB 301 CGVTSVPDIRCQLTNPNDRIILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKPAVD 360

QY 361 ARYEACNRLANKAVQSGADNVTVMVRIGH 392
DB 361 ARYEACNRLANKAVQSGADNVTVMVRIGH 392

RESULT 5
US-10-147-874-3
; Sequence 3, Application US/10147874
; Publication No. US20030027237A1
; GENERAL INFORMATION:
; APPLICANT: TARDIEUX, ISABELLE
; APPLICANT: DELORME, VIOLAINE
; TITLE OF INVENTION: SERINE-THREONINE PHOSPHATASE PROTEIN OF A PARASITIC ORGANISM OF T
; FILE REFERENCE: 22316US0
; CURRENT APPLICATION NUMBER: US/10/147,874
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/291,609
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-147-874-3

Query Match 63.3%; Score 1277; DB 14; Length 248;
Best Local Similarity 100.0%; Pred. No. 1e-111;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 LITRVSYFAVFDGGHGGIRASKFAAQNHLIRKFKGVDVSVKRCLLDTFKHTDE 200
DB 1 LITRVSYFAVFDGGHGGIRASKFAAQNHLIRKFKGVDVSVKRCLLDTFKHTDE 60

QY 201 EFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDSPRAILCRYNEESQKHAALSLSKEH 260
DB 61 EFLKQASSQKPAWKDGTATCVLAVDNILYIANLGDSPRAILCRYNEESQKHAALSLSKEH 120

QY 261 NPTQYEEEMRIQKAGNVDRGVLGVLEVSRSIGDQYKRCGVTSPDIRCQLTNPNDRI 320
DB 121 NPTQYEEEMRIQKAGNVDRGVLGVLEVSRSIGDQYKRCGVTSPDIRCQLTNPNDRI 180

QY 321 ILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAADARYEACNRLANKAVQSGA 380
DB 181 ILLACDGLFKVFTPEEAVNFILSCLEDEKIQTRGKSAADARYEACNRLANKAVQSGA 240

QY 381 DNVTVMV 388
DB 241 DNVTVMV 248

RESULT 6

US-10-072-012-853
; Sequence 853, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerrhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08

```

; Remaining Prior Application data removed - See File Wrapper or PALM.
;
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 853
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Serine/threonine phosphatases, family 2C,
; OTHER INFORMATION: catalytic domain
US-10-072-012-853

```

```

Query Match      20.9%; Score 422.5; DB 12; Length 260;
Best Local Similarity 36.4%; Pred. No. 3.5e-31;
Matches 103; Conservative 56; Mismatches 93; Indels 31; Gaps 6;

QY      105 GLKGYVAERKGEREMQDAHVILNDITEECRPSSLIITVSVFAYPFDGGHGRASKFAAQ 165
      ||: : : : : ||: : : : : ||: : : : : ||: : : : : ||: : : : :
Db       9 GLRYGKSMQGVRRKPMEDAHVITPDLSGE-----DSGGFFGVFDGGHSEAAKFLSK 60

QY      166 NLHONLIRKPKGDVISEVETIKRECLLDTFKHTDEEFLKQASSQXPAMKQSGSTATCVILAV 225
      ||: : : : : ||: : : : : ||: : : : : ||: : : : : ||: : : : :
Db      61 NUPETLAEELIKDK--DEDEDVEDALPKALRTEDEILLESLESDQ-RSGTAVVALIR 117

QY      226 DNLIYIANLGSRAILCRINEESOKHAALSLSKEHNPTQYERMRIQAGGNVDRGVLG 285
      ||: : : : : ||: : : : : ||: : : : : ||: : : : : ||: : : : :
Db     118 GNKLIVANGDSRAVLKENGK-----AVQLTDEHKPSNEDEREIRIRGAGFVSGRVNG 171

QY      286 VLEVSRTGDCQYKRCGVTSVPDIRCOLTPNDRFILLACDGLFKVFYTPPEAVNFIISCL 345
      ||: : : : : ||: : : : : ||: : : : : ||: : : : : ||: : : : :
Db     172 VLALSEALGD--FFLKPVYAEFPDVTVVELTEKDFILLASDGLWDVLSNQEWDIV---- 226

QY      346 EDEKIQTREGKSAADARYEAACNRLANKAVQGRSADNVTVWVY 388

Db     227 -----RKHLKGGPOBAKKLI DLATARGSKNIITWVVY 260

```

RESULT, T 7

US-101-170-789-35
; Sequence 35, Application US/10170789
; Publication No. US20030180930A1
; GENERAL INFORMATION:
; APPLICANT: Rachel E. Meyers
; APPLICANT: Olandt, Peter J.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Williamson, Mark
; APPLICANT: Weich, Nadine
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASE, PHOSPHATASE,
; AND PROTEASE FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-191001
; CURRENT APPLICATION NUMBER: US/10/170,789
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/797,039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: FCT/US01/06525
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/882,166
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: FCT/US01/19269
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/212,078
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 09/934,406
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: FCT/US01/26052
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,740
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/861,901

```

? PRIOR FILING DATE: 2001-05-21
? PRIOR APPLICATION NUMBER: PCT/US01/16549
? PRIOR FILING DATE: 2001-05-21
? PRIOR APPLICATION NUMBER: US 60/205,508
? PRIOR FILING DATE: 2000-05-19
? PRIOR APPLICATION NUMBER: US 09/801,267
? PRIOR FILING DATE: 2001-03-06
? PRIOR APPLICATION NUMBER: PCT/US01/07138
? PRIOR FILING DATE: 2001-03-05
? PRIOR APPLICATION NUMBER: US 60/187,454
? PRIOR FILING DATE: 2000-03-07
? PRIOR APPLICATION NUMBER: US 09/829,671
? PRIOR FILING DATE: 2001-04-10
? PRIOR APPLICATION NUMBER: PCT/US01/40483
? PRIOR FILING DATE: 2001-04-11
? PRIOR APPLICATION NUMBER: US 60/197,508
? PRIOR FILING DATE: 2000-04-18
? PRIOR APPLICATION NUMBER: US 09/961,721
? PRIOR FILING DATE: 2001-09-24
? PRIOR APPLICATION NUMBER: PCT/US01/29904
? PRIOR FILING DATE: 2001-09-24
? PRIOR APPLICATION NUMBER: US 60/235,023
? PRIOR FILING DATE: 2000-09-25
? PRIOR APPLICATION NUMBER: US 10/045,367
? PRIOR FILING DATE: 2001-11-07
? PRIOR APPLICATION NUMBER: US 60/246,561
? PRIOR FILING DATE: 2000-11-07
? PRIOR APPLICATION NUMBER: US 09/801,275
? PRIOR FILING DATE: 2001-03-06
? PRIOR APPLICATION NUMBER: PCT/US01/07074
? PRIOR FILING DATE: 2001-03-05
? PRIOR APPLICATION NUMBER: US 60/187,420
? PRIOR FILING DATE: 2000-03-07
? NUMBER OF SEQ ID NOS: 63
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 35
? LENGTH: 300
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: consensus sequence
? PS-10-170-789-35

```

```

Query Match      20.9%; Score 421.5; DB 14; Length 300;
Best Local Similarity 36.4%; Pred. No. 5.4e-31;
Matches 114; Conservative 56; Mismatches 86; Indels 57; Gaps 15;

QY      111 VAERKGEREMODAHVILNDITECRPPSSLIITRVSYFAVFDGHGGIRASKFAAQNLIHQN 170
Db      5 VSRQGWKRSNEDAHIALKNINSSSGKSW-----SFFAVFDGHS-QAAKYACKHLHKT 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      171 LI---RKFPKGD-----VISVEKTVKRCLLDTFKHTEDEELKQASS-----OKPAMKQG 216
Db      60 ILAERSFFEGDPWEMKLSOLEDAIKESFLEA--DTDEELRSASAASANKVLIKEDLSSG 117
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      217 STATCVAVDNILYIANLGDRAILCRYNNEOSOKHAALSLSKBNPTQYEEERWRIQKAG 276
Db      118 STAWALAIRGNKLYVANVGDSDRAVLCR-NGNAIKW-AVLTLEDHKPSNEDERERIEAAGG 175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      277 ---NVRDGRVLGVLEYSRSGDQYK---RCG-----VTSVPDI--RR 311
Db      176 FVSRSVNGRVNGVLAVSRAPGDFELPGSKLGPEESLEANVYIKSPQDLVTAEPDVTS 235
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      312 CQLTPN--DRFILLIACDGLFKVFTPEEAVNFIILSCLEDEKIQTEGKSAADARVEAAACNRL 370
Db      236 TDLTPDKDFLLIACDGLWDVSDQVWDIVRSELD-----GNKSAEDPMEAA-EKL 287
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      371 ANKAVORGSGADNV 383
Db      288 VDEAIARGSGEDNI 300
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 8

RESULT 10
US-10-424-599-226412
; Sequence 226412, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kowalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Sov Nucleic Acid Molecules and Other Molecules Associated With

```

Query Match      20.0%; Score 403.5; DE 12; Length 252;
Best Local Similarity 37.3%; Pred.No.2.le=29;
Matches 104; Conservative 53; Mismatches 85; Indels 37; Gaps 10;

111 VAERKGRREEMQDAHVILNIDITECPSSLITVSVFAVFDGCGGIRASKFAAQNLHQN 170
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Ddb      5 VSRVCGGRFKEFMEDIAKGNLNSGGKDSK-----GFAVFDGCGSQAKTAGHLETK 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

171 L-IRK-PFKGDIVSEKTVKRCLLDTFKHTDEEFLQASSQRPAAWKDGGSTATCVLAVDNI 228
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;; FILE REFERENCE: 38-21(53223)B
;; CURRENT APPLICATION NUMBER: US/10/424,599
;; NUMBER OF SEQ ID NOS: 285684
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 285684
;; SEQ ID NO 226412
;; LENGTH: 338
;; TYPE: PR1
;; ORGANISM: Glycine max
;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT_MRT3847_4647C.1.pap
US-10-424-599-226412

Query Match 20.0%; Score 403.5; DB 12; Length 338;
Best Local Similarity 39.2%; Pred. No. 3.2e-29;
Matches 112; Conservative 44; Mismatches 83; Indels 47; Gaps 13;
QY 109 GYAEKGEREMQDAH-VILNDITECRPPSSLLITRVSFAVFDGHHGIRASKFAAQN 167
DB 81 GY-ASSPKRSSMEDFYETKIDGVGEI-----VGLFGVFDGHHGIRAEYVKQNL 130
QY 168 HONLRKPKGDVISVEKTVKRCLLDTFKHTDEBFLKQASSQKPAWKD-GSTATCVLAVD 226
DB 131 FSNLI-SHPK--FIS---DTSAADAYNHTDSFLKSENNQ---RDAGSTASTAILVG 181
QY 227 NILYIANLGSRAILCRYNEESQKHAALSKEHNPTQYERMRIOKAGNVR---DGRV 283
DB 182 DRLLVANVGDSRAVICRGN-----AIAVSRDHKPDQTDERRIEDAGGFWWAGTW 235
QY 284 LGVLEVSISGDQYKRCGVTSVPDIRCOLTPNDIRFILLACDGLFKVFTPEEAVNFILS 343
DB 236 GGVLAVSRAFGDRLKQY-VVADPEIQEIKVDSLEFLILASDGLDGLWVNSNEEAVAMI-- 292
QY 344 CLEDEKIQTREGKSAADARYEAACNRLANKAVQSGADNVTVMVVR 389
DB 293 -----KPIEDA--EEAKRLMQEAYQSGADNITCVVVR 324

RESULT 11
US-10-424-599-219869
; Sequence 219869, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 219869
; LENGTH: 314
; TYPE: PR1
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_4056C.1.pap
US-10-424-599-219869

Query Match 19.8%; Score 399.5; DB 12; Length 314;
Best Local Similarity 39.2%; Pred. No. 6.8e-29;
Matches 112; Conservative 42; Mismatches 85; Indels 47; Gaps 13;
QY 109 GYAEKGEREMQDAH-VILNDITECRPPSSLLITRVSFAVFDGHHGIRASKFAAQN 167
DB 36 GY-ASSPKRSSMGDFYETRIDGVGEV-----VGLFGVFDGHHGIRAEYVKQNL 85
QY 168 HONLRKPKGDVISVEKTVKRCLLDTFKHTDEBFLKQASSQKPAWKD-GSTATCVLAVD 226
DB 86 FSNLI-SHPK--FIS---DTSAIDAYNHTDSLLKSENNH---RDAGSTASTAILVG 136

QY 227 NILYIANLGSRAILCRYNEESQKHAALSKEHNPTQYERMRIOKAGNVR---DGRV 283
DB 137 DRLLVANVGDSRAVICRGN-----AIAVSRDHKPDQTDERRIEDAGGFWWAGTW 190
QY 284 LGVLEVSISGDQYKRCGVTSVPDIRCOLTPNDIRFILLACDGLFKVFTPEEAVNFILS 343
DB 191 GGVLAVSRAFGDRLKQY-VVADPEIQEIKVDSLEFLILASDGLDGLWVNSNEEAVAMI-- 247
QY 344 CLEDEKIQTREGKSAADARYEAACNRLANKAVQSGADNVTVMVVR 389
DB 248 -----KPIEDA--EEAKRLMQEAYQSGADNITCVVVR 279
RESULT 12
US-10-424-599-219880
; Sequence 219880, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 219880
; LENGTH: 312
; TYPE: PR1
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_4057C.1.pap
US-10-424-599-219880

Query Match 19.7%; Score 397.5; DB 12; Length 312;
Best Local Similarity 39.3%; Pred. No. 1e-28;
Matches 112; Conservative 41; Mismatches 87; Indels 45; Gaps 12;
QY 109 GYAEKGEREMQDAH-VILNDITECRPPSSLLITRVSFAVFDGHHGIRASKFAAQN 168
DB 36 GY-ASSPKRSSMGDFYETRIDGVGEV-----BIVGLFGVFDGHHGIRAEYVKQNL 86
QY 169 HONLRKPKGDVISVEKTVKRCLLDTFKHTDEBFLKQASSQKPAWKD-GSTATCVLAVD 227
DB 87 FSNLI-SHPK--FIS---DTSAIDAYNHTDTELKSENNH---RDAGSTASTAILVG 137
QY 228 ILYIANLGSRAILCRYNEESQKHAALSKEHNPTQYERMRIOKAGNVR---DGRV 284
DB 138 RLLVANVGDSRAVICRGN-----AIAVSRDHKPDQTDERRIEDAGGFWWAGTW 191
QY 285 GVLVSISGDQYKRCGVTSVPDIRCOLTPNDIRFILLACDGLFKVFTPEEAVNFILS 344
DB 192 GVLVSRAFGDRLKQY-VVADPEIQEIKVDSLEFLILASDGLDGLWVNSNEEAVAMI-- 247
QY 345 CLEDEKIQTREGKSAADARYEAACNRLANKAVQSGADNVTVMVVR 389
DB 248 -----KPIEDA--EEAKRLMQEAYQSGADNITCVVVR 279

RESULT 13
US-09-860-351-4
; Sequence 4, Application US/09860351
; Patent No. US20020077463A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 16105, A NOVEL PROTEIN HUMAN PHOSPHATASE
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 38155-20013.00
; CURRENT APPLICATION NUMBER: US/09/860,351
; CURRENT FILING DATE: 2001-05-17

Search completed: April 12, 2004, 09:13:31
Job time : 47 secs

Best Local Similarity 37.0%; Pred. No. 1.le-27;
Matches 105; Conservative 51; Mismatches 82; Indels 46; Gaps 11;

QY 111 VABKGEREMQDAH-VILNDITEECRPSSLLITRYSFAVFDGHHGGIRASKFAAQNHLQ 169
||| : : : ||| : : : ||| : : : ||| : : :
Db 107 VASSPGKRASMEFYEARIDVDGE-----KVMFGVGDGHGVAAEYVKHLS 157

QY 170 NLRKPFGDVI SVEKTVFGLDTPKHDTDEFLKQASSQPAWKD-GSTAICVLAVDNI 228
||| : : : ||| : : : ||| : : : ||| : : :

Db 158 NLH-KHPK-----FIQDTKAAIAETNRTDSEFLKADSTQT---RDAGASTAIIVGR 208

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
Run on: April 12, 2004, 09:05:12 ; Search time 23 Seconds
(without alignments)
879.886 Million cell updates/sec
Title: US-09-935-124A-2
Perfect score: 2018
Sequence: 1 MDLFGDUPERSRPAAGK.....KAVORGADNVTVMVWVIGH 392
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 389414 seqs, 51625971 residues
Total number of hits satisfying chosen parameters: 389414
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 15 summaries
Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.psp:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.psp:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.psp:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.psp:*
5: /cgn2_6/ptodata/2/iaa/ECTUS_COMB.psp:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.psp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	2018	100.0	392	3 US-09-013-881-2 Sequence 2, Appli
2	2018	100.0	392	4 US-09-612-473-2 Sequence 2, Appli
3	340	15.8	306	2 US-08-822-701-8 Sequence 8, Appli
4	340	15.8	306	3 US-08-935-855-8 Sequence 8, Appli
5	326	15.2	390	4 US-09-206-646-4 Sequence 4, Appli
6	320.5	15.9	309	2 US-08-822-701-7 Sequence 7, Appli
7	320.5	15.9	309	3 US-08-935-855-7 Sequence 7, Appli
8	319	15.8	390	2 US-08-873-093-3 Sequence 3, Appli
9	319	15.8	390	4 US-09-206-646-3 Sequence 3, Appli
10	317.5	15.7	281	2 US-08-822-701-9 Sequence 9, Appli
11	317.5	15.7	281	3 US-08-935-855-9 Sequence 9, Appli
12	314	15.6	372	4 US-09-973-963-4 Sequence 4, Appli
13	313	15.5	478	2 US-08-873-093-1 Sequence 1, Appli
14	313	15.5	478	2 US-08-873-093-4 Sequence 4, Appli
15	313	15.5	479	4 US-09-206-646-1 Sequence 1, Appli
16	312	15.5	387	4 US-09-461-325-178 Sequence 178, App
17	312	15.5	387	4 US-10-012-542-178 Sequence 178, App
18	271.5	13.5	314	2 US-08-822-701-10 Sequence 10, Appl
19	271.5	13.5	314	3 US-08-935-855-10 Sequence 10, Appl
20	269.5	13.4	392	2 US-08-822-701-2 Sequence 2, Appli
21	269.5	13.4	392	3 US-08-935-855-2 Sequence 2, Appli
22	269.5	13.4	542	3 US-08-935-855-22 Sequence 20, Appl
23	255.5	12.7	546	3 US-08-935-855-20 Sequence 20, Appl
24	178	8.8	504	2 US-08-752-891-2 Sequence 2, Appli
25	178	8.8	504	2 US-09-144-178-2 Sequence 2, Appli
26	178	8.8	504	3 US-09-406-854-2 Sequence 2, Appli
27	178	8.8	504	4 US-09-529-279-2 Sequence 2, Appli

Sequence 2, Appli
Sequence 43, Appli
Sequence 43, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 4701, Ap
Sequence 6748, Ap
Sequence 171, App
Sequence 4777, Ap
Sequence 22696, A
Sequence 10, Appl
Sequence 10, Appl
Sequence 13, Appl
Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-013-881-2
; Sequence 2, Application US/09013881
; Patent No. 6132964
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Puri
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,881
; FILING DATE: HEREMITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BILLINGS, LUCY J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0470 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT02
; CLONE: 195647
US-09-013-881-2

Query Match 100.0%; Score 2018; DB 3; Length 392;
Best Local Similarity 100.0%; Pred. No. 1.3e-200;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRAAGKEAQKGPLLFDLPASSTDSGGPPLFDLPASSGDSG 60

Db 1 MDLFGDLPEPERSPPRAAGKEAQKGPLLFDLPASSTDSGGPPLFDLPASSGDSG 60

QY 61 SLATISQMVKTGKAKRTSBEKNGSEELVEKKVCKASSVIFGLKGVVAERKGEREE 120

Db 61 SLATISQMVKTGKAKRTSBEKNGSEELVEKKVCKASSVIFGLKGVVAERKGEREE 120

QY 121 MQDAHVLNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180

Db 121 MQDAHVLNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180

QY 181 ISVEKTVKRCCLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 240

Db 181 ISVEKTVKRCCLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 240

QY 241 LCRNEESQKHAALSLSKEHNPTQYEBMRIOKAGGNVDRGRVLGVLEVSRSIGDQYKR 300

Db 241 LCRNEESQKHAALSLSKEHNPTQYEBMRIOKAGGNVDRGRVLGVLEVSRSIGDQYKR 300

QY 301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQITREGKSAAD 360

Db 301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQITREGKSAAD 360

QY 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392

Db 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392

RESULT 2

US-09-612-473-2

; Sequence 2, Application US/09612473

; Patent No. 6518029

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Lal, Preeti

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES

; FILE REFERENCE: PF-0470-1 CIP

; CURRENT APPLICATION NUMBER: US/09/612,473

; CURRENT FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: 09/013,881

; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: PERL Program

; SEQ ID NO 2

; LENGTH: 392

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. 6518029 195647

US-09-612-473-2

Query Match 100.0%; Score 2018; DB 4; Length 392;
Best Local Similarity 100.0%; Pred. No. 1.3e-200;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLFGDLPEPERSPPRAAGKEAQKGPLLFDLPASSTDSGGPPLFDLPASSGDSG 60

Db 1 MDLFGDLPEPERSPPRAAGKEAQKGPLLFDLPASSTDSGGPPLFDLPASSGDSG 60

QY 61 SLATISQMVKTGKAKRTSBEKNGSEELVEKKVCKASSVIFGLKGVVAERKGEREE 120

Db 61 SLATISQMVKTGKAKRTSBEKNGSEELVEKKVCKASSVIFGLKGVVAERKGEREE 120

QY 121 MQDAHVLNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180

Db 121 MQDAHVLNDITECRPPSSLIITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKFPKGDV 180

QY 181 ISVEKTVKRCCLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 240

Db 181 ISVEKTVKRCCLDTFKHTDEEFLKQASSQKPAWKDGTATCVLAVDNILYIANLGSRAI 240

QY 241 LCRNEESQKHAALSLSKEHNPTQYEBMRIOKAGGNVDRGRVLGVLEVSRSIGDQYKR 300

Db 241 LCRNEESQKHAALSLSKEHNPTQYEBMRIOKAGGNVDRGRVLGVLEVSRSIGDQYKR 300

QY 301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQITREGKSAAD 360

Db 301 CGVTSVPDIRRCOLTPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQITREGKSAAD 360

QY 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392

Db 361 ARYEACNRLANKAVQSGADNVTVMVVRIGH 392

RESULT 3

US-08-822-701-8

; Sequence 8, Application US/08822701

; Patent No. 5976853

; GENERAL INFORMATION:

; APPLICANT: Guthridge, Mark

; APPLICANT: Basilico, Claudio

; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE

; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David A. Jackson, Esq.

; STREET: 411 Hackensack Ave, Continental Plaza, 4th

; STREET: Floor

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/822,701

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 1049-1-002 N

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-487-5800

; TELEFAX: 201-343-1684

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 306 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; FRAGMENT TYPE:

; ORGANISM: Rattus

US-08-822-701-8

Query Match 16.8%; Score 340; DB 2; Length 306;

Best Local Similarity 33.7%; Pred. No. 9.6e-27;

Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;

QY	106	GLKGYAERKGEREEMQDAHVILNDITECRPPSSLITRVSYFAVFDGHHGIRASKFAAQ	165
Db	21	GLRYGLSSMQGWRVEMEDAHTAVIGL-----PSGLET-WSFFAVYDGHAGSQVAKYCC	73
QY	166	NLHQLIRKFP-KGD--VISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGSTATCV	222
Db	74	HLLDHITNNQDPKGSAGAPSVN-NGKGIKRTGFLIDEHMRVMSKKHGGADRSGSTAVGV	132
QY	223	LAVDNILYIANLGDRAILCRYNESQKHAALSLSKEHNPTQYEEVRMIQKAGGNVRDGR	282
Db	133	LISPOHTYFINGDSRGLLCR-----NRKVHFFTDQHKPSNPLEKRIQAGGSVMIOR	186
QY	283	VLGVLEVSRSIGDGOYKRC-----GVT-----SVPDIRCQLTPNDRFILLACDGLFK	330
Db	187	VNGSLAVSRALGDPDYK-CVHGKGFTQOLVSPPEVHDIERSE--EDDQFILLACDGIWD	243
QY	331	VFTPEAVNFILSCLE--DEKIQTRGKSAADARYEACNRLANKAVQSGADNVTVMVY	388
Db	244	VMGNEELCDFVRSRLEVTD-----LEKVCNEVVDTCLYKGSRDNMNVILI	289
RESULT 4			
US-08-935-855-8			
; Sequence 8, Application US/08935855			
; Patent No. 6066485			
; GENERAL INFORMATION:			
; APPLICANT: Guthridge, Mark			
; APPLICANT: Basilio, Claudio			
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE			
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13			
; NUMBER OF SEQUENCES: 22			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: David A. Jackson, Esq.			
; STREET: 411 Hackensack Ave, Continental Plaza, 4th			
; STREET: Floor			
; CITY: Hackensack			
; STATE: New Jersey			
; COUNTRY: USA			
; ZIP: 07601			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/935,855			
; FILING DATE:			
; CLASSIFICATION: 435			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Jackson Esq., David A.			
; REGISTRATION NUMBER: 26,742			
; REFERENCE/DOCKET NUMBER: 1049-1-002 CIP			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 201-487-5800			
; TELEFAX: 201-343-1684			
; INFORMATION FOR SEQ ID NO: 8:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 306 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: Protein			
; HYPOTHETICAL: NO			
; FRAGMENT TYPE:			
; ORIGINAL SOURCE:			
; ORGANISM: Rattus			
US-08-935-855-8			
Query Match 16.8%; Score 340; DB 3; Length 306;			
Best Local Similarity 33.7%; Pred. No. 9,6e-27;			
Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;			
QY	106	GLKGYAERKGEREEMQDAHVILNDITECRPPSSLITRVSYFAVFDGHHGIRASKFAAQ	165

Db	21	GLRYGLSSMQGWRVEMEDAHTAVIGL-----PSGLET-WSFFAVYDGHAGSQVAKYCC	73
QY	166	NLHQLIRKFP-KGD--VISVEKTVKRCLLDTFKHTDEEFLKQASSQKPAWKDGSTATCV	222
Db	74	HLLDHITNNQDPKGSAGAPSVN-NGKGIKRTGFLIDEHMRVMSKKHGGADRSGSTAVGV	132
QY	223	LAVDNILYIANLGDRAILCRYNESQKHAALSLSKEHNPTQYEEVRMIQKAGGNVRDGR	282
Db	133	LISPOHTYFINGDSRGLLCR-----NRKVHFFTDQHKPSNPLEKRIQAGGSVMIOR	186
QY	283	VLGVLEVSRSIGDGOYKRC-----GVT-----SVPDIRCQLTPNDRFILLACDGLFK	330
Db	187	VNGSLAVSRALGDPDYK-CVHGKGFTQOLVSPPEVHDIERSE--EDDQFILLACDGIWD	243
QY	331	VFTPEAVNFILSCLE--DEKIQTRGKSAADARYEACNRLANKAVQSGADNVTVMVY	388
Db	244	VMGNEELCDFVRSRLEVTD-----LEKVCNEVVDTCLYKGSRDNMNVILI	289
RESULT 5			
US-09-206-646-4			
; Sequence 4, Application US/09206646			
; Patent No. 6436637			
; GENERAL INFORMATION:			
; APPLICANT: Bandman, Olga			
; APPLICANT: Goli, Surya K.			
; APPLICANT: Lal, Preeti G.			
; APPLICANT: Corley, Neil C.			
; APPLICANT: Zhang, Hong			
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE			
; FILE REFERENCE: PF-0319-1 DIV			
; CURRENT APPLICATION NUMBER: US/09/206,646			
; CURRENT FILING DATE: 2001-12-07			
; NUMBER OF SEQ ID NOS: 4			
; SOFTWARE: PERL Program			
; SEQ ID NO 4			
; LENGTH: 390			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc feature			
; OTHER INFORMATION: ID No. 6436637 g452526			
US-09-206-646-4			
Query Match 16.2%; Score 326; DB 4; Length 390;			
Best Local Similarity 30.0%; Pred. No. 4e-25;			
Matches 98; Conservative 52; Mismatches 121; Indels 56; Gaps 10;			
QY	78	KRTSEEEKNGSEELVEKKVCKKASSVIFGLKGYAERKGEREEMQDAHVILNDITECRP	137
Db	7	KPKTEKHNAHGAGN-----GLRYGLSSMQGWRVEMEDAHTAVVGI-----	46
QY	138	PSLITRVSYFAVFDGHHGIRASKFAAQNLHQL-----IRKFPK-GDVI--SVEKTVKR	189
Db	47	PHGL-DNWSFFAVYDGHAGSRVANYCSTHLLSHITTNEEDFRAADKSGSALEPSVE-SVKT	104
QY	190	CLLDTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDRAILCRYNESQ	249
Db	105	GIRTGFLKIDEMYRNFSDLRNGMDRSSTAVGVMSPTHTYFINGDSRGLLCRNGQ----	161
QY	250	KHAALSLSKEHNPTQYEEVRMIQKAGGNVRDGRVLGVLEVSRSIGDGOYKRCG-----	302
Db	162	---VCFSTQDHKECPNPEKRIQAGGSVMIORVNGSLAVSRALGDIYKVDGKGPSTQ	218
QY	303	-VTSVPDIRCQLTPNDRFILLACDGLFKVFTPEAVNFILSCLEDEKIQTRGKSAADA	361
Db	219	LVSPEPEVVEIVRABEDFEFVLACDGIWDVMSNEELCFVKGRLE-----VSD	266
QY	362	RYEAAACNRLANKAVQSGADNVTVMVY	388
Db	267	DLENVCNVVVDTCLYKGSRDNMNVILV	293

RESULT 6
US-08-822-701-7
; Sequence 7, Application US/08822701
; Patent No. 5976853
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilio, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,701
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; US-08-822-701-7
Query Match 15.9%; Score 320.5; DB 2; Length 309;
Best Local Similarity 29.7%; Pred. No. 1e-24;
Matches 98; Conservative 54; Mismatches 115; Indels 63; Gaps 12;
QY 78 KRKTSSEKNGSBEELVEKVKCKASSVIFGLKGYVAERKGEREMQDAHVILNDITECRP 137
Db 7 KPKEKXNAHAGN-----GLRYGLSSMQGWRVEMEDAHTAVVGI----- 46
QY 138 PSSLIITVSYFAVFDGHHGGRASKPAQNLHQL-----IRKFPK-GDVI--SVE--KTV 187
Db 47 PHGL-DNWSFFAYVDGHGGRASKPAQNLHQL-----GLRYGLSSMQGWRVEMEDAHTAVVGI 105
QY 188 KRCLDTFKHTDEFLKQASSQKPAW-KDGSTATCVLAVDNILYIANLGDRAILCRYNE 246
Db 106 RTGFLKI-----DEYRNFSDLRNGMDRSGSTAVGVNVSPTMYFINGDSRAVLCRNGQ 160
QY 247 ESQKHAALSLSKEHNPQYEEVRRIQKAGNVDRDGRVLGVLSVRSIGDQYKRCG---- 302
Db 161 -----VCFSTQDHKPCNPVEKERIQNAGGSVMIQRVNGSLAVSRALGDYKCVDGKGP 214
QY 303 -----VTSVPDIRCQLTPNDRFILLACDGLFKVFTPEEAVNFIKLEDEKIQTRGKSA 358
Db 215 TEQLVSPPEVYRIVRAEEDFVVLACDGIWDVMSNEELCFVKSRLE----- 262
QY 359 ADARYEAACNLANKAVQSGADNVTVMVV 388

Db 263 VSDDLNVNVCNWWYDVTCLHKGSRDMSVWLW 292
RESULT 7
US-08-935-855-7
; Sequence 7, Application US/08935855
; Patent No. 6066485
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilio, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,855
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; US-08-935-855-7
Query Match 15.9%; Score 320.5; DB 3; Length 309;
Best Local Similarity 29.7%; Pred. No. 1e-24;
Matches 98; Conservative 54; Mismatches 115; Indels 63; Gaps 12;
QY 78 KRKTSSEKNGSBEELVEKVKCKASSVIFGLKGYVAERKGEREMQDAHVILNDITECRP 137
Db 7 KPKEKXNAHAGN-----GLRYGLSSMQGWRVEMEDAHTAVVGI----- 46
QY 138 PSSLIITVSYFAVFDGHHGGRASKPAQNLHQL-----IRKFPK-GDVI--SVE--KTV 187
Db 47 PHGL-DNWSFFAYVDGHGGRASKPAQNLHQL-----GLRYGLSSMQGWRVEMEDAHTAVVGI 105
QY 188 KRCLDTFKHTDEFLKQASSQKPAW-KDGSTATCVLAVDNILYIANLGDRAILCRYNE 246
Db 106 RTGFLKI-----DEYRNFSDLRNGMDRSGSTAVGVNVSPTMYFINGDSRAVLCRNGQ 160
QY 247 ESQKHAALSLSKEHNPQYEEVRRIQKAGNVDRDGRVLGVLSVRSIGDQYKRCG---- 302
Db 161 -----VCFSTQDHKPCNPVEKERIQNAGGSVMIQRVNGSLAVSRALGDYKCVDGKGP 214
QY 303 -----VTSVPDIRCQLTPNDRFILLACDGLFKVFTPEEAVNFIKLEDEKIQTRGKSA 358

TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 STREET: Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/822,701
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-002 N
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 281 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM: Saccharomyces cerevisiae
 S-08-822-701-9

Query Match 15.7%; Score 317.5; DB 2; Length 281;

Query Match	15.7%	Score	317.5;	DB	2;	Length	281;
Best Local Similarity	31.4%;	Pred.	No. 1.8e-24;				
Matches	95;	Conservative	44;	Mismatches	93;	Indels	71; Gaps
			12;				
QY	111	VAERKGE--REEMODAHVILINDITEECRPPSSLIITRV--SYFAVDGHHGGTRASKFAAQN	166				
Db	23	VAENKSKFRMTMEDVHTYVNFA-----SRLDWGYPFVFDGHAGIQASKWCKH	72				
QY	167	LH----QNLIRKFPKGDIVSEKTVKRCLLDTFKHTDEEFLKQASSSQPAMKDGST--ATC	221				
Db	73	LHTTIEQNIL-----ADETRDVRDLNDSFLAIDEEI-----NTKLVGNSGCTAAVC	119				
QY	222	VL----AVDNI-----LYIANLGDSRAILCRYNESQKHAALSISKEHNPFQY	265				
Db	120	VLRMELPSVSDSDSMDLAQHQRKLYTANVGDSRIVLFRNGN-----SIRLTYDHKASDT	173				
QY	266	EERWRIQAGGNVDGVILGVLEYSRSIGDGQYKRCGVTSVPDIRRCQLTPNDPAFILLAC	325				
Db	174	LEMORVEOAGLIMKXSWNGMLVATSLGDKFFDSLWGS-PFTTSVITSEDKFLLIAC	232				
QY	326	DGLFKVFPEEAVNFILSCLEDEKIQTRECKSAADARYEAACNRANKNAVORGSDNVTV	385				
Db	233	DGLHDVIDDDQACELIKDIETPNE-----AAKLVRVIALENGTTDNVTV	276				
QY	386	MVV	388				
Db	277	MVV	279				

RESULT 11

US-08-935-855-9
; Sequence 9, Application US/08335855
; Patent No. 6066485
; GENERAL INFORMATION:

APPLICANT: Guthridge, Mark
 APPLICANT: Basilio, Claudio
 TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
 TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 STREET: Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/935,855
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 281 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM: Saccharomyces cerevisiae
 US-08-935-855-9

Query Match 15.7%; Score 317.5; DB 3; Length 281;
Best Local Similarity 31.4%; Pred. No. 1.8e-24;
Matches 95; Conservative 44; Mismatches 93; Indels 71; Gaps 12;

[illegible]

RESULT 12

REF ID: A630112
US-09-973-963-4

```

; Sequence 4, Application US/09973963
; Patent No. 6653102
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,963
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-973-963-4

```

Query Match 15.6%; Score 314; DB 4; Length 372;
Best Local Similarity 27.5%; Pred. No. 6.5e-24;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

[illegible]

RESULT 13
US-08-873-093-1
; Sequence 1, Application US/08873093
; Patent No. 5853997
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,093
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0319 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: THPIPLB01
CLONE: 13177
US-08-873-093-1

Query Match 15.5%; Score 313; DB 2; Length 478;
Best Local Similarity 28.7%; Pred. No. 1.2e-23;
Matches 94; Conservative 52; Mismatches 125; Indels 56; Gaps 8;

QY	78	KRKTSEBKNGSSELVEKKVCKKASSVIFGLKYGVABRGGEREMODAHVILNDITECRP	137
Db	7	KPKTEKINAHGAGN-----GLRYGLSSMQGWRVEMEDAHTAVVGI-----	46
QY	138	PSSJLITVSVYFAVPDGHGGIRASKFAAQNHLNLR-----KPPKGDVISEKTVKR	189
Db	47	PHGL-EDWSPFAYVDHGASRVANYCSTLLEHITTNEDFRAAGKSGSALELSVE-NVKN	104
QY	190	CLLDTXHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILXIANIGDSRATLCAYNEEQ	249
Db	105	GIRTGFLKIDYEMNFSDLUNGMDRGSGTAVGMLSPKHVIYPCINGDSRAVLYRNGQ---	161
QY	250	KHAALSLSKSHNPTQYEERMRIQKAGNVDRGVLGVLEVSRSIGDGQYKRCG-----	302
Db	162	---VCPSTQDKECNPREXERIQNAGGSMIORVNGSLAVSRALGDYDKVCDGKGPTQ	218
QY	303	-VTSVPDIRCQTPNDRTILLACDGLFKVFTPEAVNFIJSCLEDEKIQITREKSAADA	361
Db	219	LVSPEPEVYIILRAEDEFILLACDGIWDVMSNEELCEYVKSRLE-----VSD	266
QY	362	RYEACNRLANKAVQRGSDADNVTVMVV	388
Db	267	DLENVCNWWYDTCILHKGSRDNNMSIVLV	293

```

RESULT 14
US-08-873-093-4
; Sequence 4, Application US/08873093
; Patent No. 5953997
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,093
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-0319 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1452526
US-08-873-093-4

Query Match	15.5%; Score 313; DB 2; Length 478;
Best Local Similarity	28.7%; Pred. No. 1.2e-23;
Matches	94; Conservative 52; Mismatches 125; Indels 56; Gaps 8;
78 KRKTSSEKQSGBELVEKTKYKASSVIFGLKGVVAERKGEREMODAHVINDITECRP	137
7 KPKEKHNAGAGN-----GLRYGLSSMOGRVEMEDAHVAVGI-----	46
138 PSSLIITRVSPFAVFDGHHGIRASKFAAQNLHQLNR-----RFPKGDVISVEKTKR	189
47 PHGL-EDWSFVAVYDGHAGSERVANYCSTHLEHTTNEDFRAAGKSGSALSLSVE-NVKV	104
190 CLLDTFKHTDEEFLKQASOKPAWKDGSTATCVCLAVDNLITYIANLGSRAILCRYNESQ	249
105 GIR*GFLKIDBYMRNFDLRLNGMDRSGSTAVGWMISPKHIYFINGDSKAVLYRNGQ---	161
250 KHAALSLSKEHNPTQYEERNRIQKAGCNTRDGRVGLVLSRSIGDGYKRCG-----	302
162 ---VCFSTQDHKPCNPKEKRIQNAAGSGYMIQRVNGSLAVSPALGDYDYCKVDGKGPTQ	218
303 -VTSVPDIRRCQLTPNDRFILLACDGLKFVFPPEEAVNFILLSCLDEKIQTRCKSAADA	361
219 LVSPPEPVYILRAEDEFILLACDGIWDMNEELCEYVKSRLE-----VSD	266
362 RYZAACNRLANKAVQRGSDNVTVWV	388
267 DLENVCNWVVDTCCLKHGRSDNMNVLV	293

RESULT 15
US-09-206-646-1
Sequence 1, Application US/09206645
Patent No. 6436637
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Lal, preeti G.
APPLICANT: Corley, Neil C.

```

/ APPLICANT: Zhang, Hong
/
/ TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
/
/ FILE REFERENCE: PF-0319-1 DIV
/
/ CURRENT APPLICATION NUMBER: US/09/206,646
/
/ CURRENT FILING DATE: 2001-12-07
/
/ NUMBER OF SEQ ID NOS: 4
/
/ SOFTWARE: PERL Program
/
/ SEQ ID NO 1
/
/ LENGTH: 479
/
/ TYPE: PRT
/
/ ORGANISM: Homo sapiens
/
/ FEATURE:
/
/ NAME/KEY: misc_feature
/
/ OTHER INFORMATION: Incyte ID No. 6436637 013177CD1
/
/ US-09-206-646-1

```

```

Query Match      15.5%; Score 313; DB 4; Length 479;
Best Local Similarity 28.7%; Pred. No. 1.2e-23;
Matches 94; Conservative 52; Mismatches 125; Indels 56; Gaps 8;

138 PSSLTIRYSYFAVDFGHGIGIRASKEFAAQLHQLIR-----KPPKGDVISVEKTVKR 189
47 PHGL-EDWSFFAVYDGHAGSRVANYCSTHLLHEHTTNEEDFAAGKSGSALELSVE-NVKN 104
190 CLLDTFKTIDEEFLKQASQKPAWKDGGSTATCVLAVDNILYITANI.GDSRAILCRYNEESQ 249
105 GIRTGFLKIDEXYMRNFSPLRNGDMRSGSTAVGWMISPKHIYITNCDSAVLYRNQG--- 161
250 KHAALSLSKEHNPTQYERMRITQKAGGNVRDGRVLGVLEVSRSIGDGQVKRCG----- 302
162 ---VCFSTQDHKPCNPREKERIQAGGSMIQVNGSVLAVSRALGDYDYKCVDGKGPTQEQ 218
303 -VTSVPDIRRCQLTPDNDFILLACDGLFKVFTPEEAVNPFILSCLEDEKIQTREGKSAADA 361
219 LVSPEPEYVEILRAEEDFILLACDGIWDVMSNEELCEYVKSRLE-----VSD 266
362 RYEACNELANKAVORGSDNVTVMV 388
267 DLENVCNWWDTCLHKGRSDNMSIVLV 293

```

Search completed: April 12, 2004, 09:08:47
Job time : 24 secs